

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
10 May 2001 (10.05.2001)

PCT

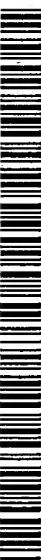
(10) International Publication Number  
**WO 01/32928 A2**

- (51) International Patent Classification<sup>7</sup>: C12Q 1/68, G01N 33/50
- (74) Agents: SHIEH-NEWTON, Terri, M. et al.; Morrison & Foerster LLP, 755 Page Mill Road, Palo Alto, CA 94304-1018 (US).
- (21) International Application Number: PCT/US00/30474
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (22) International Filing Date: 3 November 2000 (03.11.2000)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- |            |                              |    |
|------------|------------------------------|----|
| 60/165,398 | 5 November 1999 (05.11.1999) | US |
| 60/196,571 | 11 April 2000 (11.04.2000)   | US |
- (71) Applicant (*for all designated States except US*): PHASE-1 MOLECULAR TOXICOLOGY [US/US]; 2904 Rodeo Park Dr. East, Santa Fe, NM 87505 (US).
- (72) Inventor; and
- (75) Inventor/Applicant (*for US only*): FARR, Spencer [-/US]; 2904 Rodeo Park Dr. East, Santa Fe, NM 87505 (US).
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— Without international search report and to be republished upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



**WO 01/32928 A2**

(54) Title: METHODS OF DETERMINING INDIVIDUAL HYPERSENSITIVITY TO AN AGENT

(57) Abstract: Methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes associated with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes associated with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes for the plurality of genes associated with hypersensitivity. The expression of the genes predetermined to be associated with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases arrays and apparatus useful for identifying hypersensitivity in a subject are also disclosed.

## METHODS OF DETERMINING INDIVIDUAL HYPERSENSITIVITY TO AN AGENT

### TECHNICAL FIELD

5       The invention generally relates to methods, compositions and devices for identifying individuals who are hypersensitive to a given agent.

### BACKGROUND OF THE INVENTION

Individuals exhibit a high degree of variability in their response to chemicals, 10 including pharmaceutical compounds. A major concern of pharmaceutical manufacturers is that a subset of the patient population may display significant toxic side effects that cannot be predicted from preclinical studies. In many cases this hypersensitivity results in extreme, and even lethal, responses. The incidence of serious and lethal adverse reactions to drugs among hospitalized patients in the United States causes at least 100,000 deaths per 15 year. This makes adverse responses to therapeutic drugs the fifth main cause of death in the United States.

The existence of a hypersensitive sub-population is usually only discovered after a compound has been broadly prescribed and a population base of sufficient size has had exposure to the compound. These same drugs are generally safe for the majority of 20 individuals and most respond favorably to the desired effects of the drugs. In many cases, the same drug that may elicit severe toxic responses in a subset of the population is the best drug for the particular disease being treated. For example, clozapine is a very effective drug for treating moderate to severe depression and with the majority of patients shows no toxic side effects at the recommended doses. Yet at the same dose (usually 300 mg), 25 approximately 1% of the patient population develop agranulocytosis, a severe blood disorder.

Many compounds have either been withdrawn from the market altogether or severely restricted in use due to severe adverse responses by a subset of the patient population. In some instances, it is known that a subset of the population is hypersensitive, and physicians are advised to be alert for indications of extreme toxic response in such patients. Exemplary compounds include tienilic acid, halothane, dihydrazine, diclofenac, fialuridine, carbamazepine, Trovan<sup>TM</sup> (trovafloxacin), Seldane<sup>TM</sup> (terfenadine), hismanol, dihydrolazine, warfarin, phenytoin, omeprazole, diazepam, haloperidol, perphenazine, perhexiline, phenformin, tolbumamide, penicillin, clozapine, aminopurine, quinidine and remoxipide.

Unfortunately, in the vast majority of these cases, there is no way of identifying a hypersensitive individual before prescribing the drugs or exposing the worker to the compound. Hypersensitive individuals are discovered the hard way; they exhibit toxic side effects that most people do not. Furthermore, since the mechanisms of toxicity are specific and usually different for each drug or compound, the hypersensitive populations are also different and specific for each drug or compound.

When an approved drug is found to elicit serious toxicity in only a subset of the population the manufacturer is usually required to tightly restrict access to the drug, carefully monitor all patients who receive the drug for toxic side effects, or withdraw it from the market altogether. A high number of compounds also fail in the late stages of development because of serious toxicity in a subset of the clinical trial population. When a drug is found to cause severe toxicity in a sub-population, besides the trauma and pain for such hypersensitive individuals, there is great financial loss incurred by the manufacturer. The cost to the manufacturer of withdrawing or restricting a compound can be billions of dollars in lost market capitalization, legal liabilities and unrecoverable research and development expenses. Adverse reactions are becoming the main challenge for pharmaceutical research and development. (Drug Discovery Today) 4:393-395 (1999). In

addition, very effective drugs are often pulled from the market and thus become unavailable to those who would benefit greatly from them.

It would save lives, decrease pain and suffering and save pharmaceutical manufacturers and consumers a great deal of money if there were a way to determine in advance which individuals were likely to experience severe toxic responses to a drug.

### SUMMARY OF THE INVENTION

Disclosed herein are methods, gene databases, gene arrays, protein arrays, and devices that may be used to determine the hypersensitivity of individuals to a given agent, such as a drug or other chemical, in order to prevent toxic side effects.

In one embodiment, the invention relates to a method of identifying hypersensitivity in a subject by obtaining the gene expression profile of specific genes associated with hypersensitivity of the subject suspected to be hypersensitive and identifying in the gene expression profile of the subject a pattern of gene expression of the genes associated with hypersensitivity. The gene expression profile of the subject may be compared with the gene expression profile of individuals who have an acceptable response and compared with other hypersensitive individuals. The embodiment also includes, for example, identifying hypersensitivity to an agent in a subject, where the agent may be a pharmaceutical agent, industrial, household or other chemical or compound. Exemplary pharmaceutical agents are disclosed in Table 1.

The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes complementary to the genes associated with hypersensitivity. The genes used may comprise at least two genes, at least 3, 4, 6, 7, 8, or 9 genes predetermined to be associated with hypersensitivity, and may also comprise at least 5, at least 10, at least

25, at least 50, at least 100, at least 250 or more genes determined to be associated with hypersensitivity.

Genes associated with hypersensitivity and used in this invention may, for example, comprise genes from a variety of different cell types, including, but not limited to, genes  
5 from multiple types of tissues, organs or systems or genes from a single type of tissue, organ or system. Exemplary organs and tissues include the liver, kidneys, heart, brain, thyroid, lung, pancreas, muscle, brain, testes, ovaries, spleen, stomach, intestines, colon, rectum, eyes, muscle, skin, and bone. Exemplary types of cells include liver cells such as, Kupfer cells, sinusoidal cells, ito cells, hepatocytes, bile duct epithelial cells, hepatic venule  
10 endothelial cells and sinusoidal epithelial cells.

A further embodiment encompasses the expression profile of the genes predetermined to be associated with hypersensitivity where expression of the genes is related to prevention or repair of toxic damage at the nucleotide, protein, macromolecule, organelle, cell, tissue, organ or system level.

15 In another embodiment, the gene expression profile may comprise a profile of protein expression levels, where the proteins are encoded by genes associated with hypersensitivity. The level of expression of the proteins may be directly related to the prevention or repair of toxic damage at the protein, nucleotide, macromolecule, organelle, cell, tissue, organ or system level. An additional embodiment includes protein expression  
20 profiles, where the proteins are encoded by genes associated with hypersensitivity, and the expression of the genes is, for example, associated with response to the presence of an agent, such as a toxic agent. Exemplary agents that can induce a characteristic profile of protein expression associated with hypersensitivity include those agents listed in Table 1.

The gene expression profile may be obtained from a sample from the subject, which  
25 sample may be from a cell or tissue sample and may comprise cells of different cell types. For gene expression, the sample may comprise, for example, white blood cells, skin, spinal

fluid or organ biopsy material. For protein expression analysis, the sample may comprise, for example, blood, tissue, urine, spinal fluid or serum.

In another embodiment, cells or tissues derived from an individual are used to establish primary cell cultures, for example fibroblasts, hepatocytes, and other examples known in the art. These primary cell cultures are then exposed to the agent. Co-cultures are also encompassed in the invention and are grown from two or more cell types that reflect, for example, the cell types involved in systemic toxicity. These co-cultures would then be exposed to the agent of interest.

In another embodiment, the gene expression profiles of samples from normal individuals, hypersensitive individuals or cell cultures are determined for individual agents using the methods herein described to determine drug-drug interactions. The gene expression profiles are compared to determine whether the multiple agents, for example two or more agents, elicit the same or similar gene expression profiles in the samples. The expression of the same or similar pattern(s) of toxic response genes for two or more compounds in either normal or hypersensitive individuals, is indicative that a drug-drug interaction, also described as a synergistic toxic effect, can be present if the agents are administered together, for example, during the same time period or in the same dose.

The genes used in the gene expression profile may include, but are not limited to, genes, and the proteins which they encode, which are associated with toxic outcomes affecting the pulmonary system, cardiovascular system, nervous system, digestive system, immune system, reproductive system, endocrine system, vision or skin. Exemplary types of toxicity include cardiotoxicity, blood toxicity, liver (hepatic) toxicity, kidney (renal) toxicity, neural toxicity, skin toxicity, immunotoxicity, and pulmonary toxicity. Exemplary genes associated with specific organ or system toxic outcomes are disclosed in Table 5.

The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, altered lipid

metabolism, altered thyroid function, organ hypertrophy, skin irritation, skin sensitization, tumor formation, dementia, inflammation, myelosuppression, peripheral neuropathy, necrosis, signal refractivity, spreading, transformation, retinopathy or optic atrophy.

The genes used in the gene expression profile may include, but are not limited to 5 genes, and the proteins which they encode, which are associated with toxic outcomes affecting the digestive system or the organs and tissues which comprise the digestive system, for example, the liver, kidneys, colon, bladder, pancreas, stomach, intestines, rectum, or gallbladder.

The genes used in the gene expression profile include those genes, and the proteins 10 which they encode, associated with exemplary toxic outcomes such as, but not limited to, proteinuria, glomerulitis, nephritis, renal damage, renal failure, liver weight change, cholestasis, pancreatitis, liver steatosis, hyperplasia, fatty liver, jaundice, hepatitis, mutagenesis, or altered bile flow.

The genes used in the gene expression profile may include, but are not limited to 15 genes, and the proteins which they encode, which are associated with toxic outcomes affecting the pulmonary system or the organs and tissues which comprise the pulmonary system, for example the lungs or trachea.

The genes used in the gene expression profile include those genes, and the proteins 20 which they encode, associated with toxic outcomes such as, but not limited to, lung fibrosis, pulmonary edema or lung airway reactivity.

The genes used in the gene expression profile may include, but are not limited to 25 genes, and the proteins which they encode, which are associated with toxic outcomes affecting the cardiovascular and circulatory systems or the organs, fluids and tissues which comprise the cardiovascular and circulatory systems, for example, the heart, spleen, arteries, blood vessels, blood or blood cells, including genes associated with toxic outcomes associated with bone marrow.

The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with exemplary toxic outcomes such as, but not limited to, tachycardia, arrhythmia, leukemia, neutropenia, hematological alteration, hypotension, hypertension or agranulocytosis.

5 The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the nervous system or the organs and tissues which comprise the nervous system, for example, the brain, spinal cord or nerves.

10 The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, neurodegeneration or neurotoxicity.

15 The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the immune system or the organs and tissues which comprise the immune system, for example, the thymus, lymph nodes or lymph glands.

The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, a change in thymic weight or immunosuppression.

20 The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the reproductive system or the organs and tissues which comprise the reproductive system, for example the testes, ovaries, fallopian tubes or uterus.

25 The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, teratogenesis, loss of fertility, alteration in sperm count, alteration in testes weight or alteration in testosterone levels.

The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with cellular manifestations of toxicity such as, but not limited to, apoptosis, cell adhesion, autophagocytosis, cell division, chemotaxis, cell cycle arrest, circadian rhythm, cytokine release, differentiation, de-differentiation, mitochondrial damage, migration, mutation, oncosis, recombination, senescence, peroxisome proliferation, polyploidy, signal refractivity, spreading, transformation or necrosis.

5 The genes involved, and the proteins which they encode, may also include those associated with a specific ethnic group, sex or age group.

10 The genes or proteins used in the expression profile may also include the genes, and the proteins or amino acids which they encode, which are selected from the genes disclosed in (or genes comprising sequences disclosed in) Table 3, Table 4, Table 5, Table 6, Table 8, Table 10 and Table 11.

15 In another embodiment, the method includes obtaining a gene expression profile of genes comprising different cell types, of the subject, determining if the gene expression profile of the subject comprises a pattern of gene expression associated with hypersensitivity to an agent, and withholding that agent from those subjects who are hypersensitive or altering the therapy and closely monitoring the subjects who are hypersensitive for toxic effects.

20 In another embodiment, a method of identifying a plurality of genes associated with hypersensitivity to an agent is provided, comprising comparing the gene expression profile of cells treated with an agent with the gene expression profile of cells not treated with the agent and identifying genes that have altered expression due to exposure to the agent in the treated cells. The cells may comprise, for example, a number of different cell types and each cell type may comprise a gene associated with hypersensitivity to the agent. The cells 25 may also comprise cells from of different cell types where all the cell types are derived from a single type of tissue, organ or system. The organs or tissues from which cell types

may be derived include, but are not limited to, the kidneys, liver, lungs, heart, brain, spleen, thyroid, bone, muscle, intestine, stomach, pancreas, testes, ovaries, colon or skin.

The invention also relates to a method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent by comparing the  
5 gene expression profile of one or more cell types, for example, at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100 or at least 250, of a subject known to be hypersensitive to the agent with the gene expression profile of the cell types in an individual known not to be hypersensitive to the agent and identifying genes from the two or more cell types which exhibit a pattern of differential gene expression associated with  
10 hypersensitivity to the agent.

In an alternative embodiment, the method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent comprises comparing the gene expression profile of one or more cell types, for example, at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100 or at least 250, of a subject known to  
15 be hypersensitive to the agent before treatment with the agent with the gene expression profile of the one or more cell types of the subject after treatment with the agent and identifying genes from the cell types having a pattern of differential gene expression associated with hypersensitivity to the agent.

In an alternative embodiment, the method of identifying proteins having a pattern of differential protein expression indicative of hypersensitivity to an agent comprises comparing the protein expression profile of one or more cell types of a subject known to be hypersensitive to the agent before treatment with the agent with the protein expression profile of the one or more cell types of the individual after treatment with the agent and identifying proteins from the cell types having a pattern of differential protein expression  
25 associated with hypersensitivity to the agent.

In another embodiment, there is provided an array for the identification of a gene expression profile indicative of a hypersensitivity to an agent which comprises gene probes,

for example, nucleic acid sequences which comprise a gene sequence associated with hypersensitivity to the agent, associated with the hypersensitivity to the agent. The genes are selected from the genes identified by methods disclosed herein or are selected from those genes disclosed in whole or in part in Table 3, Table 4, Table 5, and Tables 6, 8, 10  
5 and 11. The array comprises for example, at least 5, at least 10, at least 25, at least 50, at least 100, at least 150, at least 250 different gene probes. Exemplary arrays include, for example, gene probes supported on glass slides or nylon membranes with fluorescent or radio labels, amplified fragment length polymorphism (AFLP) methods or Northern Blots.

The invention further encompasses a database of genes associated with hypersensitivity to an agent. The genes are those identified by methods disclosed herein or are selected from those genes disclosed in whole or in part in Table 3 and Table 4, Table 5 and Tables 6, 8, 10 and 11. The database of genes may comprise, for example, genes associated with altered lipid metabolism, cholestasis, immunosuppression, pancreatitis, agranulocytosis, tumor formation, teratogenesis, liver steatosis, apoptosis, cell adhesion,  
10 autophagocytosis, cell cycle arrest, circadian rhythm, cytokine release, differentiation, migration, oncosis, recombination, senescence, signal refractivity, spreading, transformation, peroxisome proliferation, necrosis, glomerulitis, nephritis, arrhythmia, hypotension, hypertension, leukemia, neutropenia renal damage, renal failure, pulmonary edema, neurotoxicity or retinopathy.  
15

20 The invention further encompasses a method for identifying individuals who may be hypersensitive to the toxic side effects of drugs such as those listed in Table 1 or industrial compounds such as those listed in Table 2.

An additional embodiment includes an apparatus for identifying hypersensitivity in a subject comprising means for obtaining a gene expression profile of a number of genes  
25 associated with hypersensitivity of the subject suspected to be hypersensitive; and means for identifying in the gene expression profile of the subject a pattern of gene expression of

the genes associated with hypersensitivity, thereby to identify hypersensitivity in the subject.

Also provided are methods of determining hypersensitivity of an individual to an agent, such as a pharmaceutical drug, such as penicillin, by detecting a gene expression or protein expression profile of the individual, wherein the genes or proteins encoded therefrom are selected from genes listed in whole or in part in Tables 10 and 11. The pattern of expression may be detected in a cell, such as an immune cell, such as a leukocyte, e.g. a lymphocyte.

Also provided are devices for detection of gene expression profiles comprising nucleic acid sequences for detecting expression of the nucleic acids disclosed in the Tables, for example by hybridization. Such devices include, for example, immobilized nucleic acid arrays.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a graph illustrating gene expression changes associated with toxicity caused by streptozotocin.

Figure 2 is a graph illustrating co-induction of genes for hepatocyte growth factor receptor and glutathione transferase.

Figure 3 is a graph illustrating a portion of a gene expression profile from heart muscle tissue after exposure to the cardiotoxin, doxorubicin.

Figure 4 is a graph illustrating a portion of a gene expression profile from liver tissue after exposure to the peroxisome proliferation caused by WY 14,643.

Figure 5 is a graph illustrating a portion of a gene expression profile from liver tissue after exposure to the anti-neoplastic compound, carbamazepine.

Figure 6 is a chart illustrating the result of testing for penicillin hypersensitivity amongst a group of penicillin sensitive and penicillin refractive individuals by using a 180 gene penicillin array.

Figure 7 is a chart illustrating the result testing for penicillin hypersensitivity amongst a group of penicillin sensitive and penicillin refractive individuals by using a 20 gene penicillin array.

5 Figure 8 is a chart illustrating 20 discriminator genes analyzed for co-regulation.  
Figure 9 is a graph illustrating the results of a Taqman® assay in a penicillin sensitive person.

Figure 10 is a graph illustrating the results of a Taqman® assay in a penicillin refractive person.

10

#### BRIEF DESCRIPTION OF THE TABLES

Table 1 is a list of pharmaceutical agents which potentially can cause greatly heightened toxic responses in some individuals.

15 Table 2 is a list of industrial agents which potentially can cause greatly heightened toxic responses in some individuals.

Table 3 is a list of genes, altered expression patterns of which can indicate and render an individual hypersensitive to drugs and chemical agents.

Table 4 is a list of genes, altered expression patterns of which can indicate and render an individual hypersensitive to drugs and chemical agents.

20 Table 5 is a list of genes associated with specific manifestations of organ or system toxicity.

Table 6 is a list of genes that can be associated with specific cellular manifestations of toxicity.

25 Table 7 lists compounds for which gene expression data in either human cells, rats or both has been generated.

Table 8 lists genes whose expression was measured when rats were exposed to the cardiotoxin doxorubicin.

Table 9 lists cell types in organs of toxicity.

Table 10 lists the characterization of genes which were isolated and sequenced from gel bands.

Table 11 lists the genes that are useful discriminator genes.

5

#### DETAILED DESCRIPTION OF THE INVENTION

Provided are methods, compositions and apparatus for identifying hypersensitivity  
10 in an individual. In one embodiment, hypersensitivity in a subject is determined by obtaining from the subject a sample from which can be determined the gene expression profile of genes associated with hypersensitivity, and identifying in the gene expression profile the presence or absence of a pattern of gene expression of the genes associated with hypersensitivity, thereby to identify hypersensitivity in the individual.

15

#### General Techniques

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are within the skill of the art. Such techniques are explained fully in the literature, such as, *Molecular Cloning: A Laboratory Manual*, second edition (Sambrook *et al.*, 1989); *Oligonucleotide Synthesis* (M.J. Gait, ed., 1984); *Animal Cell Culture* (R.I. Freshney, ed., 1987); *Handbook of Experimental Immunology* (D.M. Weir & C.C. Blackwell, eds.); *Gene Transfer Vectors for Mammalian Cells* (J.M. Miller & M.P. Calos, eds., 1987); *Current Protocols in Molecular Biology* (F.M. Ausubel *et al.*, eds., 1987); *PCR: The Polymerase Chain Reaction*, (Mullis *et al.*, eds., 1994); *Current Protocols in Immunology* (J.E. Coligan *et al.*, eds., 1991); *The Immunoassay Handbook* (David Wild, ed., Stockton Press NY, 1994); *Antibodies: A*

*Laboratory Manual* (Harlow et al., eds., 1987) and *Methods of Immunological Analysis* (R. Masseyeff, W.H. Albert, and N.A. Staines, eds., Weinheim: VCH Verlags gesellschaft mbH, 1993).

5      Definition of Terms

As used herein, the terms ‘gene’, ‘polynucleotide’, ‘nucleotide’ and ‘nucleic acid’ are interchangeable and refer to polynucleotide sequences, which for example, encode protein products and encompass mRNA, cDNA, single stranded DNA, double stranded DNA and fragments thereof.

10     The terms “protein”, “polypeptide”, and “peptide” are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non-amino acids. It also may be modified naturally or by intervention; for example, disulfide bond formation, glycosylation, myristylation, acetylation, alkylation, phosphorylation or dephosphorylation.

15     Also included within the definition are polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids) as well as other modifications known in the art.

20     The terms ‘stress gene’, ‘toxicity gene’ and ‘toxic response gene’ as used herein are interchangeable. A toxic response gene can be defined as a gene whose message or protein level is altered by adverse stimuli. The specific set of genes that cells induce is dependent upon the type of damage or toxic threat caused by the agent and which organs are most threatened. In addition to the up-regulation of genes which respond to specific toxic threat, genes which encode functions not appropriate under conditions of toxic injury may be down-regulated.

25     As used herein, ‘toxic outcome’ refers to the microscopic or macroscopic symptoms, physiological, morphological or pathological changes which are observed as a result of exposure to an agent.

A 'toxic response' as used herein refers to a cellular, tissue, organ or system level response to exposure to an agent and includes, but is not limited to, the differential expression of genes and/or proteins encompassing both the up- and down-regulation of such genes; the up- or down-regulation of genes which encode proteins associated with the repair or regulation of cell damage; or the regulation of genes which respond to the presence of an agent.

A 'gene expression profile associated with hypersensitivity' as used herein refers to the pattern of relative levels of gene expression found to be associated with hypersensitivity. Gene expression profiles may be measured in a sample, such as samples comprising a variety of cell types and may, for example, comprise blood, urine, spinal fluid or serum.

A 'protein expression profile associated with hypersensitivity' is defined as the pattern of relative levels of protein expression where said proteins are encoded by genes determined to be associated with hypersensitivity. For each gene expression profile that is determined, a corresponding 'protein expression profile associated with hypersensitivity' may be determined.

The terms 'up-regulation' and 'induction' are used interchangeably herein and refer to the regulation of gene expression, specifically the turning on of a particular gene(s). Similarly, the terms 'down-regulation' and 'repression' are used interchangeably herein and refer to the suppression of expression of a particular gene(s).

An 'agent' to which an individual is hypersensitive is defined as any substance to which an individual may be hypersensitive and includes, but is not limited to, drugs, household chemicals, industrial chemicals and other chemicals and compounds to which individuals may be exposed.

'Hypersensitivity', as used herein, refers to the exaggerated micro- or macroscopic responses of cells, tissues, organs or systems to low or average doses of an agent. These responses may lead to observable symptoms such as dizziness or nausea and can also result

in toxic outcomes. Hypersensitivity often results in toxic side effects that are different, in either degree or kind, from the response of the majority of patients at the recommended dose. Hypersensitivity may be characterized by, but is not limited to, the differential expression of genes when compared to the response of a similar individual who is not hypersensitive to a given agent. Hypersensitive individuals do not have normal gene expression patterns of key toxicologically relevant genes either prior to, or after, exposure to an agent.

5       ‘Differential expression’ as used herein refers to the change in expression levels of genes, and/or proteins encoded by said genes, in cells, tissues, organs or systems upon exposure to an agent. As used herein, differential gene expression includes differential transcription and translation, as well as message stabilization. Differential gene expression encompasses both up- and down-regulation of gene expression.

10      The term ‘individual’ is used interchangeably with the term ‘subject’ and ‘patient’ and refers to a mammal, preferably the primate, more preferably the human.

15      The term ‘normal individual’ or ‘normal subject’ refers to individuals who exhibit the same or similar dose response curves to an agent as does the majority of the exposed population. Most drugs at high enough dosages will cause a toxic response, therefore a ‘normal toxic response’ refers to the toxic response elicited in an average or normal individual at high doses of an agent.

20      The term ‘sample’ as used herein refers to samples for testing or analysis. The samples may comprise cells or tissue samples and may be, for example, blood, urine or serum. Samples are characterized in a preferred embodiment by comprising at least two different genes and may also include genes from multiple cell types. Samples include, but are not limited to, those of eukaryotic, mammalian or human origin.

25      As used herein, “array” and “microarray” are interchangeable and refer to an arrangement of a collection of nucleotide sequences in a centralized location. Arrays can be on a solid substrate, such as a glass slide, or on a semi-solid substrate, such as

nitrocellulose membrane. The nucleotide sequences can be DNA, RNA, or any permutations thereof. The nucleotide sequences can also be partial sequences from a gene, primers, whole gene sequences, non-coding sequences, coding sequences, published sequences, known sequences, or novel sequences.

5 "Penicillin sensitive" refers to individuals who exhibit hypersensitivity to penicillin, for example, a higher than average immune response to penicillin. The immune response can be a hypersensitive response of any type, for example Type I, II, III, or IV. Hypersensitive reactions can include but are not limited to anaphylaxis, skin rash, and hives. Hypersensitive responses also include hypertoxicity.

10 "Penicillin refractive" or "penicillin insensitive" or "penicillin non-sensitive" as used herein refers to individuals who exhibit a normal or non-hypersensitive response to penicillin.

#### Isolating DNA/RNA from human PBL

15 Nucleotide sequences from human peripheral blood lymphocytes (PBL) are isolated using any number of commercially available kits i.e. from Qiagen, GenHunter, Promega, etc.

In one embodiment, total RNA is isolated from tissue samples using the following materials: Qiagen RNeasy midi kits, 2-mercaptoethanol, liquid N<sub>2</sub>, tissue homogenizer, dry ice. It is important to take precautions to minimize the risk of RNA degradation by RNases by wearing gloves at all times and to inhibit RNase activity in work areas and equipment by treating with an RNase inhibitor such as with "RNase Zap" (Ambion® Products, Austin, TX). Autoclaving tips and microfuge tubes does not necessarily eliminate RNase enzymes and its RNA degradation activities. Samples are kept on ice when specified . Protocol 20 which can be used is based on Qiagen® RNeasy® midi kit. This total RNA isolation technique is used for RNA isolation from human PBL and can be modified readily by one 25 of skill in the art to accommodate different amount of human PBLs. The human PBL is

preferably taken from circulating blood of a human donor. However, human PBL can also be obtained from lymph nodes, spleen, and other tissues into which human PBLs circulate.

If tissue containing human PBL is used, then the tissue needs to be microdissected. One way is to physically break the tissue by placing it on a double layer of aluminum foil 5 which is then placed within a weigh boat containing a small amount of liquid nitrogen. The aluminum foil is folded around the tissue and then the tissue is struck by a small foil-wrapped hammer to administer mechanical stress forces.

To preserve integrity of the RNA, all tissues are kept on dry ice when other samples are being weighed. A buffer is added to the sample to aid in the homogenization process.

10 An example of a buffer which can be used is RLT (Qiagen®) buffer. The tissue is homogenized using any type of commercially available homogenizer (i.e. IKA Ultra Turrax T25 homogenizer, Virtishear Cyclone 750W rotor/stator homogenizer (Virtis item # 278077, etc.) can be used with the 7 mm microfine sawtooth shaft and generator (195 mm long with a processing range of 0.25 ml to 20 ml, item # 372718). After homogenization, 15 samples are stored on ice until all samples are homogenized. The homogenized tissue sample can then be spun to remove nuclei thus reducing DNA contamination. The supernatant of the lysate is then transferred to a clean container containing an equal volume of 70% EtOH in DEPC treated H<sub>2</sub>O and mixed. In the event that a stringy white material comes out of solution, it may then be removed. RNA is isolated by putting the supernatant 20 through an RNeasy spin column, washed, and subsequently eluted.

In another embodiment, DNA or RNA is isolated from human PBLs obtained from a human donor. Generally, lymphocytes can be isolated from blood by separating the blood over a gradient, for example a sucrose gradient or Percoll™ or Ficoll™ gradient. Lymphocytes can be distinguished from non-lymphocyte contaminants by morphology, 25 size and scatter by flow cytometry, or by cell surface markers such as CD2, CD3, CD4, or CD8. In general, lymphocytes which are cultured *in vitro* are non-adherent but in some instances, lymphocytes can be adherent or non-adherent depending on several factors, for

example, activation state of lymphocytes, receptors expressed on lymphocytes, and culture media contents. In some aspects, adherent cells are more problematic than non-adherent cells because of the necessity of an extra step to separate the adherent cells from the tissue culture container. However, a skilled artisan may solve this problem by treating the cells with cold PBS/EDTA solutions or an equivalent and use any number of commercially available kits, for example, from Qiagen or Ambion, to isolate the DNA or RNA from the cells. In one embodiment, total RNA of high quality and high purity can be isolated from cultured cells by using Qiagen RNeasy midi kits and 2-mercaptoethanol. This embodiment is exemplified in Example 2 *infra*. Precautions should be taken to minimize the risk of 5 RNA degradation by RNases by wearing gloves, treating work areas and equipment with an RNase inhibitor, for example RNase Zap (Ambion® Products, Austin, TX), and keeping samples on ice. Using a Qiagen® RNeasy® midi kit (50), this total RNA isolation technique can be used for any type of cell, including but not limited to human lymphocytes and cell derived from particular organs such as kidney, liver, lung, breast, neuronal cells, 10 skin, intestine, such as HepG2, Caco-2, MCF-7, Jurkat, Daudi, HL-60, MCL-5, SKBr-3, SKOV-3, PC-3, WISH, and HeLa.

To practice this embodiment, cells are checked under the microscope to confirm 20 viability. Cells are then dosed with an agent, which can be a drug, chemical, or pharmaceutical composition, when they reach confluence. In a preferred embodiment, the cells are at least about 20% confluent, more preferably at least about 40% confluent, even more preferably at least about 60% confluent, and even more preferably about 80% confluent. It is preferable to avoid isolating RNA from flasks that have reached 100% confluence because the cells are no longer growing in log phase.

The adherent cells are washed and freshly prepared buffer, for example RLT buffer 25 (RLT buffer requires the addition of 10 µl beta mercaptoethanol for each 1.0 ml RLT), is added directly to the cell culture flask. The amount of RLT buffer differs with tissue container size. Enough RLT buffer is added to cover the surface area in which the adherent

cells are growing such that most of the adherent cells come into contact with the RLT buffer. In one embodiment, T-75 flasks receive about 3 ml RLT buffer and T-175 flasks receive about 5 ml RLT buffer. It is preferable to lightly agitate the flasks at this point. Cells exposed to RLT buffer become a gelatinous layer. The cells are allowed to sit for 4 minutes, then fluid is withdrawn and is placed into an RNase-free tube. An equivalent volume of 70% ethanol is added to each tube and vortexed to distribute evenly. In the event that a precipitate with a string-like appearance forms, it is acceptable to remove and discard this string-like precipitate. The fluid is applied to a spin column, centrifuged, and the column is washed and subsequently eluted for RNA samples. The elution can be precipitated using the LiCl precipitation protocol and resuspended in RNA storage buffer for future storage. The yield can be between 200-400 µg of total RNA from a T-75 flask with greater than 50% confluency.

The isolated DNA or RNA is amplified to generate a product which can be attached to a substrate. In a preferred embodiment, the substrate is a solid substrate (i.e. glass slide). The amplification process involves using primers which have a reactive group (i.e. amine group or derivative thereof) on one end of the primer, which is incorporated into the amplification product. One example of reactive primers that can be used is Amine Primers from Synthegen. The gene fragments which are attached to the glass slide can vary in length. The more nucleotides of a gene that are in the array, the tighter the binding and the greater the specificity in binding can occur. However, it is important to consider that longer fragments are more difficult to amplify and may contain point mutations or other errors associated with amplification. Therefore, the desired length of a gene or a fragment thereof that is to be included in the array should take into consideration the balance between a high specificity of binding obtained with a long (i.e. >1 kb) gene sequence with the high mutational rate associated with a longer fragment. The gene fragments attached to the glass slide are at least about 50 base pairs (bp) in length, more preferably at least about 100 bp in length, more preferably at least about 200 bp, even more preferably at least about 25

300 bp, even more preferably at least about 400 bp, even more preferably at least about 500 bp in length. In a preferred embodiment, the gene fragments are about 500 bp in length. The region of a gene that is used to attach to a solid substrate to generate an array can be any portion of the gene, coding, non-coding, 5' end, 3' end, etc. In a preferred 5 embodiment, about 500 base pairs of the 3' end of canine gene related to toxicological responses are selected to be included in an array.

Several techniques are well-known to a skilled artisan for attaching a gene or a fragment thereof to a solid substrate such as a glass slide. One method is to attach an amine group, a derivative of an amine group, another group with a positive charge or 10 another group which is reactive to one end of a primer that is used to amplify a gene or a gene fragment to be included in the array. Subsequent amplification of a PCR product will then incorporate this reactive group onto one end of the product. The amplified product is then contacted with a solid substrate, such as a glass slide, which is coated with an aldehyde or another reactive group which will form a covalent link with the reactive group 15 that is on the amplified PCR product and become covalently attached to the glass slide.

Other methods using amino propyl silicane surface chemistry are disclosed by Corning Company at <<http://www.cmt.corning.com>> other methods for making microarrays which are readily accessible at <<http://cmgm.stanford.edu/pbrown/>>

In one embodiment of the invention, fluorescence-labeled single strand (or "first 20 strand") cDNA probe is made from total or mRNA by first isolating RNA from control and treated cells, disclosed *supra*. This probe is hybridized to microarray slides spotted with DNA specific for toxicologically relevant genes. This is exemplified in Example 8-14. The materials needed to practice this embodiment are: total or messenger RNA, primer, Superscript II buffer, dithiothreitol (DTT), nucleotide mix, Cy3 or Cy5 dye, Superscript II 25 (RT), ammonium acetate, 70% EtOH, PCR machine, and ice. The Cy™ dyes may be obtained from Amersham. The embodiment may also be practiced with equivalents of the

materials listed above, for example, SuperScript II may be replaced with an equivalent enzyme and Cy5 and Cy3 may be replaced with another fluorescent dye.

In one embodiment, a discrete amount of RNA, for example 20 $\mu$ g of total RNA or 2 $\mu$ g of mRNA, is used to generate cDNA. In a preferred embodiment, the volume is no more than 14  $\mu$ l. If RNA is too dilute, the samples are concentrated to a volume of less than 14  $\mu$ l in a centrifuge with vacuum (i.e. Speedvac) without heat. The Speedvac should be capable of generating a vacuum of 0 Milli-Torr so that samples can freeze dry under these conditions. It is preferable for the tubes containing RNA to be kept on ice to avoid RNA degradation until the next step is ready to proceed. Following standard techniques well-known in the art, cDNA samples are amplified from RNA templates. A mixture of fluorescent dyes is made for labeling the cDNA samples. A variety of dyes can be used. In one embodiment, Cy3 dye, which is pink-red, and Cy5 dye, which is blue, are used. The Cy dyes are light sensitive, therefore, any solutions or samples containing Cy-dyes should be kept out of light, i.e. cover with foil. Example 9-12 discloses preferred mixtures and methods of using Cy3 and Cy5 dyes for labeling cDNA samples and purification steps therewith.

In an embodiment wherein the sequences of toxicologically relevant genes are not known and canine cells are divided into two groups, untreated and treated, to identify toxicologically relevant genes as disclosed *infra*, Cy3 dye mixture is incubated with the cDNA of each treated sample and Cy5 dye mixture is incubated with the cDNA of each control sample. Following the methods disclosed in Example 9, a visible pellet can be seen which is pink/red for cDNA incubated with Cy3 and blue for cDNA incubated with Cy5. It is recommended that the tubes are centrifuged at a fixed position so the pellet will be at a known area in the tube. In some rare instances, the cDNA sample (or cDNA probe) is seen spread on one side of the tube instead of a tight pellet. If the pellet is white (no pink/red or blue), it is likely that the reaction has not occurred to maximal efficiency.

Purification of fluorescent probes

Purification of fluorescence-labeled first strand cDNA probes can be achieved in one embodiment using the following materials: Millipore MAHV N45 96 well plate, v-bottom 96 well plate (Costar), Wizard DNA binding Resin, wide orifice pipette tips for 200 5 to 300  $\mu$ l volumes, isopropanol, and nanopure water. It will be evident to a skilled artisan that equivalent products may be substituted in other embodiments, i.e. other types of tissue culture plates, binding resin from other commercially available sources, for example Qiagen. Plate alignment during centrifugation is important since misaligned plates can lead to sample cross contamination and/or sample loss. In one embodiment, probes are purified 10 by binding to a resin. The binding resin can be obtained by itself or from a kit provided by any number of commercial sources, i.e. Qiagen, Promega, etc.

Fluorescence Readings of cDNA Probe

Incorporation of fluorescence into cDNA probes can be achieved by using a number 15 of methods. In one embodiment, the following material is used: 384 well, 100  $\mu$ l assay plate (Falcon Microtest cat#35-3980) and Wallac Victor 1420 Multilabel counter (or equivalent). Prior to use as a cDNA probe in hybridization, cDNA probes are purified and concentrated as exemplified in Example 10.

It is preferable that a consistent amount of cDNA is pipeted into the plate wells 20 because readings can vary with volume. Controls or identical samples can be pooled at this step, if required or desired. The Cy-3 and Cy-5 fluorescence are analyzed using a fluorimeter, luminometer, flow cytometer, or any equivalent device which can detect different fluorescent dyes at different wavelengths. In a preferred embodiment, the Wallac 1420 workstation programmed for reading Cy3-Cy-5 is used. A typical range for Cy-3 25 (20 $\mu$ g) is 250-700,000 fluorescence units. A typical range for Cy-5 (20 $\mu$ g) is 100-250,000 fluorescence units. Preferred settings for the Wallac 1420 fluorescence analyzer are as follows:

Cy3

CW lamp energy = 30445  
Lamp filter = P550 slot B3  
5 Emission filter= D572 dysprosium slot A4  
Emission aperture = normal  
Count time = 0.1 s

Cy5

10 CW lamp energy = 30445  
Lamp filter = D642 samarium slot B7  
Emission filter= D670 slot A8  
Emission aperture = normal  
Count time = 0.1 s

15

After detection of the cDNA probes, it is important to concentrate the cDNA probes so that they can be resuspended in hybridization buffer at an appropriate volume for hybridizing to the array. Internal normalization is achieved by taking into consideration the ratio of Cy5 fluorescence to Cy3 fluorescence in the treated and untreated canine cell groups, respectively.

20

Microarray Hybridization

Hybridization of labeled cDNA probes to single stranded, covalently bound DNA target genes on glass slide microarrays can be accomplished by a variety of methods. In 25 one embodiment, exemplified in Example 7, the following material are used: formamide, SSC, SDS, 2 µm syringe filter, salmon sperm DNA, hybridization chambers, incubator, coverslips, parafilm, and heat blocks. It is preferable that the array is completely covered to ensure proper hybridization. Hybridization buffer is prepared with consideration towards stringency. Stringency can be varied by increasing or decreasing the amount of 30 SSC and detergent (i.e. SDS, Triton, etc.). Stringency can also be varied by the temperature at which the hybridization occurs. A higher temperature tends towards high stringency conditions. A skilled artisan can determine, in a stepwise fashion, the stringency of the hybridization buffer desired. Clean slides and coverslips are desirable and can be

obtained using N<sub>2</sub> stream. Hybridization buffer is added to dried probe and mixed in the dark at room temperature and then brought to a higher temperature in a heat block. Each probe can remain in a heat block until it is ready for hybridization. The probe is applied to a slide or to a coverslip and then covered with slide. It is highly preferable to avoid the material at the bottom of the tube and to avoid generating air bubbles. This may mean leaving some residual volume in the pipette tip. Slides are then placed in a hybridization chamber, wrapped to prevent the liquids from desiccating. One problem that can occur with overly dried slides is increased fluorescence on the edge of the spot containing the target gene fragment to which the labeled cDNA probe binds. In an alternative, the hybridization chamber can have a built-in humidity gauge to avoid desiccation of the slides. In a preferred embodiment, the slides are placed in a 42°C humidity chamber in a 42°C incubator for 18 to 24 hours. It is preferable to avoid probes or slides sitting at room temperature for long periods.

15     Post-Hybridization Washing

To obtain single stranded cDNA probes on the array, all non-specifically bound cDNA probe should be removed from the array. In one embodiment, removal of all non-specifically bound cDNA probe can be accomplished by washing the array using the following materials: slide holder, glass washing dish, SSC, SDS, and nanopure water. Equivalents of SSC and SDS may also be used as substitutes. It is highly preferable that great caution be used with the standard wash conditions since deviations can affect data significantly.

In one embodiment, glass buffer chambers and glass slide holders are filled with heated SSC buffer with sufficient volume to submerge the microarrays. It is important to exercise caution in heating of the SSC buffer since a high temperature may strip off the probes, preferably the temperature is at most about 60°C, more preferably at most about 50°C, even more preferably at most about 40°C, and even more preferably at most about

35°C. A skilled artisan can vary the concentration of SSC in the buffer according to the stringency desired. The slides are placed in buffer which may contain SSC and/or detergent (i.e. SDS, Triton, etc.) and the coverslips are dislodged and fall off the slide within several minutes of submersion. In the event that the coverslips do not fall off within 5 several minutes of submersion, very gentle agitation may be administered to the chamber in which the wash is being conducted to dislodge the coverslips. The slides with the hybridized probes are subjected to several rounds of washes with different conditions. In one embodiment, a detergent (i.e. SDS) is added to the wash buffer in different concentrations and the slides are washed in this buffer before a final wash in nanopure 10 water. The slides are dried in a manner that will minimize background signal of the array. A preferred method of drying is to use a folded paper towel underneath the slide and a gently dabbing motion on the slide with a tissue. It is important that the slides do not air dry since this will lead to increased background.

15 Gene Expression Profiles

The pattern of gene expression characteristic of hypersensitivity is predetermined, and is, for example, provided in a database. By comparing the gene expression profile of the subject with the predetermined pattern of gene expression of multiple genes characteristic of hypersensitivity, the hypersensitivity of the subject can be conveniently 20 and rapidly determined. Advantageously, the invention provides a large number of predetermined gene expression patterns of genes associated with hypersensitivity, for example in a database, so that a large number of genes can be rapidly analyzed and compared in the subject. Analysis of information about expression of a wide spectrum of genes associated with hypersensitivity facilitates the rapid determination of hypersensitivity 25 of a subject to an agent, or multiple agents.

For example, the differential gene expression profile associated with a given agent can be determined for a given agent using, for instance, eukaryotic or mammalian cells or

cell lines or animal models and exposing a population of the eukaryotic or mammalian cells or cell lines or animal models to an agent and comparing their gene expression to the same type of eukaryotic or mammalian cells or cell lines or animal models from an untreated population to determine the gene expression profile associated with hypersensitivity.

5       Hypersensitivity to an agent, for example, a pharmaceutical drug or household, industrial or other chemical, can be rapidly determined with samples from an individual or group of individuals by treating the sample(s) with an agent and comparing the gene expression profile with the gene expression profile associated with hypersensitivity determined previously for a particular agent and, for instance, stored in a database and  
10      accessed and compared with associated software.

Table 1 lists approximately 200 drugs sold in the U.S. and Europe. There are individuals who are hypersensitive to the toxic side effects of each of these drugs. Table 2 lists at least 100 major industrial chemicals for which there is documented evidence of toxicity due to occupational exposure. For each of these chemicals there are individuals  
15      whose toxic response is heightened compared to the majority of the population.

In a preferred embodiment, multiple genes are analyzed. Preferably, the number of genes, associated with hypersensitivity, whose expression levels are determined and which comprise the gene expression profile is large; for example, one or more, at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, or at least 250. The present  
20      invention also encompasses gene expression profiles where the number of genes is greater than 400, 500, 600 or more.

In another embodiment, the genes, whose expression levels comprise the gene expression profile, are drawn from a variety of cell types.

For example, the genes, whose expression levels comprise the gene expression  
25      profile, are drawn from cells of a number of different tissues or organs.

In another embodiment, cells or tissues derived from an individual are used to establish primary cell cultures, for example fibroblasts, hepatocytes, and other examples

known in the art. These primary cell cultures are then exposed to the agent. Cell cultures established from the appropriate tissues of hypersensitive individuals are more sensitive to the toxic effects of the agent than cultures established from normal individuals. This hypersensitivity is reflected in the gene expression patterns elicited from the cell cultures.

5 In another embodiment, cells or tissues derived from an individual are used to establish primary cell cultures, for example fibroblasts, hepatocytes, and other examples known in the art. Co-cultures would be grown from two or more cell types that reflect the cell types involved in systemic toxicity. These co-cultures are then exposed to the agent of interest. Cell co-cultures established from the appropriate tissues of hypersensitive  
10 individuals are more sensitive to the toxic effects of the compound than co-cultures established from normal individuals. This hypersensitivity is reflected in the gene expression patterns elicited from the cell co-cultures.

In another embodiment, the gene expression profile consisting of the expression levels of multiple genes includes genes drawn from a single cell, tissue or organ type, and  
15 the profile is examined to determine the association of the gene expression profile with hypersensitivity.

In addition to the determination of absolute levels of expression for the genes in the gene expression profile associated with hypersensitivity, the relative expression levels of two or more genes in the gene expression profile associated with hypersensitivity can be  
20 determined and can be relevant to a determination of hypersensitivity. Hypersensitive individuals will have profiles of expression of relevant toxicity genes that are distinct from individuals who are not hypersensitive.

In another embodiment, gene expression profiles from normal individuals, hypersensitive individuals or cell cultures are established for individual agents to determine  
25 possible toxic drug-drug interactions when patients (normal or hypersensitive individuals) are treated with multiple drugs. There are hundreds of combinations of compounds that are more toxic when taken together than when taken singly. Usually these toxic drug-drug

interactions are discovered as clinical manifestations once the drugs reach market.

Examples of compounds that cause severe toxicity when taken together include cyclosporin A and trimethoprim, Walworth *et al.* (*Lancet*) 1:336(1983); and Clonidine and Tricyclic antidepressants such as Amoxapine. Briant *et al.* (*Br J Pharmacol*) 46:563(1972). The

5 expression of the same pattern of toxic response genes for two or more compounds in either normal or hypersensitive individuals, indicates that the two or more compounds, taken together, will often show a synergistic toxic effect. Gene expression profiles for each compound, determined *in vitro* or *in vivo*, allows prediction of the severe toxicity if the two compounds were taken together.

10 In another embodiment, the gene expression profile of genes associated with certain disease states is analyzed. Normal individuals can become temporarily hypersensitive to the toxicity of certain drugs because of disease states. Hypersensitivity is present in normal individuals when toxic defense mechanisms are temporarily compromised. For example, an individual who suffers from AIDS-induced immunosuppression will be hypersensitive 15 to the toxic effects of immunosuppressive compounds such as cyclosporin A. An individual suffering from pulmonary edema due to viral infection will be temporarily hypersensitive to compounds such as bleomycin which elicit pulmonary edema as a toxic side-effect.

20 In another embodiment, the method includes obtaining a protein expression profile of a number of proteins encoded by genes of the subject, determining if the protein expression profile of the subject comprises a pattern of protein expression associated with hypersensitivity to an agent, and withholding the agent from those individuals or altering the therapy or dosage and closely monitoring the individual for toxic effects.

25 In addition, a method of identifying a number of genes associated with hypersensitivity to an agent is provided comprising comparing the protein expression profile, where the proteins are encoded by the genes identified as associated with hypersensitivity to the agent, of cells treated with the agent with the protein expression

profile of cells not treated with the agent and determining proteins that have altered expression due to the exposure to the agent in the treated cells. The cells may comprise, for example, a variety of different cell types and each cell type may comprise a gene associated with hypersensitivity to the agent, and the protein encoded by gene.

5 An additional embodiment includes a method of identifying a number of genes associated with hypersensitivity to an agent which comprises comparing the protein expression profile, where the proteins are encoded by the genes identified as associated with hypersensitivity to the agent, of cells treated with the agent with the protein expression profile of the same type of cells from the same subject not treated with the agent and  
10 determining proteins that have altered expression due to exposure to said agent in the treated cells. The cells may comprise, for example, a variety of different cell types and each cell type may comprise a gene associated with hypersensitivity to the agent, and the protein encoded by the gene.

15 In a further embodiment, the gene expression profile of multiple genes associated with cellular response to toxic agents are analyzed to determine the association with hypersensitivity of the genes in the profile.

Using the methods, compositions and devices disclosed herein, rapid, accurate and inexpensive tests of an individual can be conducted in order to confirm whether the individual is hypersensitive to an agent. For example, an individual can be screened for  
20 hypersensitivity to a drug before the drug is administered. Such screenings avoid incidents of hypersensitivity in individuals to whom a drug might otherwise be administered. Alternately, the drug can be given in lower doses to hypersensitive individuals and/or those individuals considered at risk may be closely monitored for adverse reactions to the agent. Avoiding exposing hypersensitive individuals to any given drug or compound, or to a  
25 higher than necessary dose or level of the drug or compound, provides cost savings to manufacturers who may produce the drug or compound with an assurance that hypersensitivity reactions will be avoided. Those who are not hypersensitive may safely

receive the drug or compound and receive its benefits, while those who are hypersensitive may safely avoid the drug or be prescribed a different drug or in the case where the toxicity is due to exaggerated pharmacological effects, a smaller, but just as effective dose.

The invention also encompasses using the methods, composition and devices disclosed herein for rapid, accurate and inexpensive tests that can be used, for instance, to determine the causative agent in an individual exhibiting symptoms consistent with or indicative of a toxic response or hypersensitivity to various agents. By ascertaining the gene profile of a number of genes associated with particular cells, tissues, organs or systems, the agent eliciting the toxic response or hypersensitivity may be determined and thereon avoided. In one embodiment, gene expression analysis might be used to determine the nature of the toxic insult and thus provide treatment. For example, analysis of expression of tox-response genes might aid in the effective diagnosis and treatment of an unconscious child suspected of having been inappropriately exposed to a drug or chemical agent. Gene expression patterns could be useful in determining if the unconscious state were the result of exposure to a soporific agent or one that inhibited mitochondrial function, the treatments of which would be quite distinct.

Exemplary genes associated with hypersensitivity whose expression may be screened in order to determine hypersensitivity are provided in whole or in part in Tables 3, 4, 5, 6, 8, 10 and 11. Also provided herein are methods of identifying genes associated with hypersensitivity.

### Genes

Tables 3, 4, 5, 6, 8, 10 and 11 provide a list of exemplary genes from which genes associated with hypersensitivity to a particular agent may be selected. Genes selected from Table 3 and Table 4 are responsive to toxic stimuli and important to the defense or repair of toxic damage. Individuals with significantly altered expression levels of two or more of the genes in Tables 3, 4, 5, 6, 8, 10 and 11 can also show different toxic responses from normal

individuals. For a given agent, the expression profile of two or more genes, for example, selected from Tables 3, 4, 5, 6, 8, 10 and 11 can be obtained from a cell, tissue or organ and, a pattern of gene expression predetermined to be associated with hypersensitivity can be established.

5       Genes such as those selected from Tables 3 and 4 are evaluated for differential gene expression, for example in the major toxic target organs in humans and/or rats and mice. Examples of genes in which differential expression is indicative of toxicity or hypersensitivity in specific organs or systems such as liver (hepatic), kidney (renal), lung (pulmonary), central nervous system (neural), heart (cardio) and immune system are shown  
10      in Table 5.

As an example, Figure 1 shows the pattern of gene expression of approximately 250 genes in the liver when the subject received a relatively high dose of streptozotocin. Samples, including for instance, blood, urine, serum or tissue, from individuals known to be hypersensitive to streptozotocin can be obtained after the subject is treated with  
15      streptozotocin. Alternately, for example, samples may be from untreated individuals known to be hypersensitive to streptozotocin and the samples may then be treated *in vitro* with streptozotocin. The samples are then examined to identify genes associated with hypersensitivity. This may show, for example, highly exaggerated expression of toxic response genes and/or patterns of induction or repression of genes in treated individuals or  
20      upon *in vitro* treatment of the sample with streptozotocin compared to individuals who are not hypersensitive or sample which is not treated with streptozotocin. As streptozotocin is an example of a bulky alkylating agent, individuals who are hypersensitive to streptozotocin may be tested for hypersensitivity to compounds with similar toxic properties, such as bulky alkylating agents, such as merbarone and carmustine.

25      Genes whose levels of expression change in response to toxic stimuli may be evaluated. Examples of genes with expression changes in response to toxic stimuli are listed in Tables 3 and 4. The genes in Table 3 and Table 4 have been shown to be induced

in either cell lines, primary cells, tissues or tissue slices, from human or animal origin. For example, the GADD 153 gene has been shown to be induced in many human cell lines upon exposure to radiation. The environmentally important compound trichloroethylene was recently demonstrated to cause induction of several genes, including c-Myc and c-Jun 5 in mice exposed to low toxic levels for 24 hr. Tao et al.(J Biochem Mol Toxicol) 13(5): 231-7 (1999). In primates, closely related to humans, hyperoxia causes increased expression of the genes encoding thioredoxin and thioredoxin reductase gene expression in lungs. Das et al., (Chest) 116(1 Suppl): 101S (1999).

Many of the genes in Tables 3 and 4 are known to be involved in the prevention or 10 repair of damage to DNA, cells or tissue in response to toxic agents (several examples are provided by the following references: Kegelmeyer et al. (Mol. Carcinog.) 20(3): 288-97 (1997); Koerber et al. (Mol. Reprod. Dev.) 49(4): 394-9 (1998); Kuhn (Nutr. Rev.) 56:11-9, discussion 54-75 (1998); Lu et al. (Mol. Carcinog.) 20(2): 204-15 (1997); Muhlenkamp 15 et al. (Toxicol. Appl. Pharmacol.) 148(1):101-8 (1998); Melhus et al. (Biochem. Mol. Biol. Int.) 43(5):1145-50 (1997); Pentecost (Steroid Biochem. Mol. Biol.) 64(1-2):25-33 (1998); Quattrochi et al. (Arch. Biochem. Biophys.) 349(2):251-60 (1998); Rout et al. (Cell Calcium) 22(6): 463-74 (1997); Sadekova. et al (Int. J. Radiat. Biol.) 72(6): 653-60 (1997); Yuan et al. (J. Biol. Chem.) 273(7):3799-802 (1998); Zhao et al. (Oncogene) 16 (3):409-15 (1998).

Table 6 shows a set of genes associated with specific types of cellular toxicity. 20 Studies of single gene expression have shown over- or under- expression of certain of these genes, to affect the sensitivity of the cell or organism to toxic stimuli and are described in the art. Advantageously, the expression levels of all of these genes can be measured simultaneously. Individuals hypersensitive to an agent can be identified by measuring the expression patterns of the toxicity genes specific to that agent. Tables 3, 4, 5 and 6 are 25 non-limiting examples of such toxicity genes.

Agents

Many compounds are toxic at a high enough concentration. For example, while most individuals might experience extreme tachycardia after receiving a very high dose – 20 times normal – of a drug, they experience no such effects at recommended doses. The 5 hypersensitive individual would experience extreme tachycardia at the recommended dose or at a lower than normal dose. A hypersensitive individual might also experience a qualitatively distinct toxic response to a compound, not just the same response that a normal individual would experience at high doses. For example, the hypersensitive patient might experience extreme dizziness, a side effect not reported by individuals even at high 10 doses.

Agents to which individuals may be hypersensitive, and for which hypersensitivity can be determined, may include, for example, drugs, industrial chemicals, household or other chemicals, including those in the workplace. Examples of drugs and industrial chemicals for which a sub-population is hypersensitive are listed in Tables 1 and 2.

15 As a further example, individuals who are employed in manufacturing or other environments which expose them to a variety of agents may be screened for agents to which they might come into contact. Individuals, or for example, a subset of workers, who are hypersensitive to the agents can then be identified. Hypersensitivity to other agents also may also be determined, such agents including, but not limited to biological agents 20 such as naturally occurring organic compounds, including proteins, saccharides and lipids.

Exemplary pharmaceutical agents include, for example, tienilic acid, halothane, dihydrazine, diclofenac, fialuridine, carbamazepine, Trovan<sup>TM</sup> (trovafloxacin), Seldane<sup>TM</sup> (terfenadine), hismanol, dihydrolazine, warfarin, phenytoin, omeprazole, diazepam, haloperidol, perphenazine, perhexiline, phenformin, tolbumamide, penicillin, clozapine, 25 aminopurine, quinidine and remoxipide. Table 1 lists additional agents for which there are individuals who demonstrate hypersensitivity.

Examples of other chemicals include industrial chemicals, such as paint, volatile organic compounds (VOCs), solvents, adhesives, pesticides, herbicides, perfumes, aerosols, cleaning compounds and synthetic polymers such as textiles.

5        Identification of Genes

Genes initially suspected of being associated with hypersensitivity and hence potentially useful in the present invention are identified, for example, by conducting extensive literature searches; investigating known biochemical pathways with toxicological relevance; and measuring gene expression from toxin-exposed animals, humans or cell lines. Hypersensitivity to an agent, such as a drug, may also be determined based on the ability to identify the underlying molecular basis for the toxicity of specific drugs. Hypersensitivity can also be determined by examining the gene expression of hypersensitive and normal individuals.

In one embodiment, methods are provided wherein literature reports on the expression levels of single genes in response to a single agent are collected, for example, in a database, and then analyzed to establish patterns of expression that can be correlated to hypersensitivity. Advantageously, large amounts of data can be collected and analyzed, for example by software means. For example, Matrix Express<sup>TM</sup>, and Chem Profiler<sup>TM</sup> (Phase-1 Molecular Toxicology, Santa Fe, NM) accommodate capture and analysis of gene expression profiles. For example, it allows identification of induced genes from the total set of genes measured using a number of criteria; for example, statistical significance, two-fold, and 1.5 X the standard deviation. The software also allows the search of other profiles and determines the commonality between subsets, ranking profiles by several measures of similarity, for example, using all or a subset of the genes.

25        Experiments include both *in vivo* and *in vitro* responses to agents, for example, the exposure of eukaryotic, mammalian or human cells, and animals to agents listed in Table 7.

One ultimate benefit of this exercise is to reduce the need for animal testing. Each agent is tested at several concentrations and time points.

The toxicology of an agent is evaluated by measuring toxic insult by detecting observable changes in organ or system appearance and/or function, at the micro- or 5 macroscopic levels. For example, a drug may cause changes in fatty acid metabolism in liver hepatocytes. This in turn causes observable changes in liver appearance, such as a specific toxicological outcome referred to as fatty liver. In order for cells, and thus tissues and organs, to undergo observable morphological changes due to toxic insult, they generally express a subset of genes differently than untreated cells. Thus, manifestations of 10 toxic injury frequently require differential gene expression. Such genes that are differentially expressed in response to toxic injury are evaluated for use as genes associated with hypersensitivity in accordance with the present invention.

Thus, the expression of genes that are differentially expressed in total across cell, organ and tissue types in humans, in particular in response to toxic insult, may be evaluated 15 to determine which genes have expression that is linked to hypersensitivity in an individual. Individuals who do not properly express the appropriate toxicity response genes for a specific compound will be hypersensitive to the toxic effects of that compound.

Organs are composed of tissues, which in turn are composed of various cell types. There is a core set of genes whose products are involved in functions essential to all cells, 20 and whose expression is shared by most human cell types. In addition to these common core genes, each cell type expresses a set of genes that is unique to that cell type. When animals, including humans, are exposed to chemicals that cause damage to one or more organs, cells that comprise those organs attempt to mitigate or repair that damage by turning on genes that encode toxic-damage defense or repair proteins. The specific set of 25 genes that cells induce is dependent upon the type of damage or toxic threat caused by the compound and upon which organs are most threatened. In addition to the genes that are induced to deal with the specific toxic threat, there may be genes which encode functions

that are not needed nor appropriate under conditions of toxic injury. Therefore, both the up- and down-regulation of genes can be measured in order to understand the molecular response to that compound, and the linkage of gene expression to hypersensitivity. The pattern of differential gene expression within the toxic target organs can be limited to a  
5 relatively small number of genes, and may be very specific to both the organ being threatened and the type of damage. Such genes may be analyzed to determine which genes are responsible for hypersensitivity, for example, within a certain organ. Such genes may be analyzed to identify subsets of genes that are associated with hypersensitivity to certain agents.

10       The measurement of gene expression patterns is useful because many factors can affect the level of transcripts of toxicity genes, including mutations in the regulatory regions of genes, mutation in transcription factor that control the gene(s) of interest, and gene duplications and deletions. Examples of genes whose expression may be screened for association with hypersensitivity to certain agents are further discussed herein.

15       Genes associated with changes in expression levels due to adverse stimuli or toxic insult include, for example, genes which respond to the presence of a compound, and genes which respond to damage caused by a compound at, for example, the protein, nucleotide, macromolecular, membrane, cell, tissue, organ or system level. For example, certain proteins either prevent or repair toxic cellular injury. Individuals who do not express the  
20 appropriate gene profile will suffer greater damage from toxic compounds through a lack of repair enzymes.

25       Toxic responses can be measured by pathological changes, for example, at the protein, nucleotide, cell, tissue, organ or system level. These pathological changes can be associated with differential gene expression of at least two genes. In addition, and the correspondence between the pathological change and the differential gene expression can be established. At the concentration where pathological outcomes are observable, gene expression changes are specific and causally related to the outcome. For example,

compounds that cause peroxisome proliferation as observed in the electron microscope, such as WY 14,643 (Sigma Chemicals; St. Louis, MO), a common toxicological compound known in the art, turn on genes causally related to peroxisome proliferation (See Figure 4). Compounds that cause DNA damage as manifested by increased mutations and cell-cycle disruption turn on genes required to alter the cell cycle and repair the damage (See Figure 5 below). Furthermore, since most drugs elicit pleiotropic effects, and are metabolized differently, there is a specific gene expression pattern for each compound, even though there may be a sub-pattern with all compounds that, for example, alkylate DNA at the O-4 position of thymine.

10           Genes associated with hypersensitivity also may be identified by examination of the gene expression profile of hypersensitive individuals differing from normal gene expression patterns of the genes associated with differential gene expression either before or after exposure to the particular drug in question.

15           Genes which may be identified and tested for their association with hypersensitivity to a certain agent include a variety of genes known in the art that are induced in mammalian or eukaryotic cells or cell lines exposed to high concentrations of chemicals. Genes associated with toxicological response that can be identified for predicting different types of hypersensitivity to different agents include, for example, those genes described in: Cattell (Semin. Nephro.) 19(3):277-87 (1999); Schnabel, M. et al. (Int. J. Mol. Med.) 1(3):593-5 (1998); Cruse et al. (Carcinogenesis) 20(5) 817-824 (1999); Fogg, S. et al. (Am. J. Respir. Cell Mol. Biol.) 20(4):797-804 (1999); Aoki et al. (FEBS Lett.) 333:114-118 (1993); Feuerstein et al. (Can. J. Physiol. Pharmacol.) 75(6):731-4 (1997); Rodrigo et al. (Scand. J. Gastroenterol.) 34(3):303-307 (1999); Schmidt et al. (Biochem. Biophys. Res. Commun.) 242: 529-533 (1996); Rockett et al. (Eur. J. Drug Metab. Pharmacokinet.) 22: 239-233 (1997); Rudat et al. (Int. J. Radiol. Bio.) 73: 325-330 (1998); Buters et al. (Proc. Natl Acad. Sci USA) 96(5): 1977-1982 (1999); Wang et al. (Cardiovasc. Res.) 35

:414-421 (1997); Pang et al. (*Ann. Hum. Genet.*) 62(3): 271-4 (1998); and Herrlich, et al. (*Biol. Chem.*) 378(11):1217-29 (1997).

Many toxic response genes are induced to higher levels of expression only when needed. An individual can show a defective or hypersensitive response if a crucial protein 5 is defective or is not produced in sufficient abundance when needed. Thus individuals who do not synthesize sufficient amounts of key proteins or produce defective proteins required to minimize the toxic damage from a given agent will suffer from greater toxic injury.

Altered levels of the gene products of the genes listed in Table 3, Table 4, Table 5 and Table 6 are likely to render the cell or organism hypersensitive to toxic stimuli, and 10 there is great variability among the population in basal and induced levels of these genes. There have been many studies of some of these individual genes in the literature, some of which are discussed below. For example, a mouse knock-out mutant for the DNA repair gene PARP was shown to be hypersensitive to the toxicity and genetic damage caused by gamma-irradiation and MNU. Trucco C. et al. (*Mol Cell Biochem*) 193(1-2): 53-60 15 (1999). Humans with low basal or induced expression of the PARP gene will be hypersensitive to gamma-irradiation, MNU and all radiomimetic agents.

In another example, it was recently shown that DNA repair methyltransferase (Mgmt) knockout mice are hypersensitive to the toxic effects of several chemotherapeutic alkylating agents. Glassner et al. (*Mutagenesis*) 14(3): 339-47 (1999). Individuals with 20 decreased expression of the Mgmt gene will be hypersensitive to the same compounds.

In another example, a ‘temporary’ knock-out of the cyclophilin-A gene in mice was made by injecting an anti-sense RNA against the cyclophilin A gene in rat neonatal cardiomyocytes. The expression level of the cyclophilin A gene was reduced by 93% and animals treated were hypersensitive to the toxic effects of t-butylhydroperoxide. Doyle et 25 al. (*Biochem. J.*) 341( 1):127-32 (1999). Humans who show depressed levels of cyclophilin A gene expression are expected to be hypersensitive to the toxic effects of t-butylhydroperoxide and other compounds that form active oxygen radicals.

5 Polymorphisms occur in the human population for the gene encoding serum paraoxonase (PON1). The PON1 gene product plays a major role in the detoxification of organophosphate (OP) compounds. One polymorphism (Arg192 isoform) hydrolyzes diazoxon, soman and sarin slowly. Costa et al. (Chem. Biol. Interact) 119-120: 429-38 (1999).

10 Genes associated with hypersensitivity can be selected from those in Table 3, which are induced by toxic damage and have important physiological roles in responding to toxic stimuli. For example, Rettie et al. (Epilepsy Res.) 35(3):253 (1999) showed that humans carrying a polymorphism that decreases expression of the CYP2C9 gene are very sensitive to compounds such as phenytoin and (S)-warfarin. The data demonstrate that the 15 CYP2C9\*3 polymorphism gene product retains only 4-6% of the metabolic efficiency of the wild-type protein CYP2C9\*1 towards phenytoin and (S)-warfarin. Individuals who show dramatically reduced expression of the normal CYP2C9\*1 could show the same hypersensitivity to these drugs.

15 Several factors can affect the basal and induced levels of expression of these genes. For example, mutations or polymorphisms that affect the promoter region of tox-response genes can cause hypersensitivity to compounds. For example, several polymorphisms have been identified in the promoter region of the human HLA-DQA1 gene that affect the levels of mRNA and thus protein levels of the HLA haplotype. Indovina, P. 20 et al. (Hum. Immunol.) 59(12): 758-67 (1998). Polymorphisms in the regulatory region of the genes encoding plasminogen activating inhibitor increase the risk for developing coronary heart disease (Grenett et al. (Arterioscler. Thromb. Vasc. Biol.) 19(11):1803-1809 (1998). The polymorphisms mentioned above for human plasminogen activating inhibitor are in the regulatory region of the gene and result in altered expression of the gene. This 25 risk of developing coronary heart disease, and likely increased risk to drugs with cardiotoxic properties, is increased specifically as a function of the altered expression levels. Many toxic stimuli induce or repress TGF- $\beta$ 1 levels. Individuals who overexpress

TGF- $\beta$ 1 show heightened levels of apoptosis and fibrosis seen with mycotoxin-induced liver injury. Cruse et al. (Carcinogenesis) 20(5):817-824 (1999).

Polymorphisms in the gene encoding the vitamin D receptor change differential expression of many downstream genes and render the individual likely to develop drug induced psoriasis. Park et al. (Arterioscler Thromb Vasc Biol) 19(11):1803-1809 (1999). Expression levels of the gene for cytochrome P450 CYP1B1 have a strong effect on the susceptibility to 7, 12-dimethylbenz[a]anthracene-induced lymphomas. Thus individuals who do not express appropriate levels of the P450 CYP1B1 gene would be at enhanced risk for toxic side effects of compounds like 7, 12-dimethylbenz[a]anthracene that are metabolized by that P450 protein. Butlers et al. (Proc. Natl. Acad. Sci. USA) 96(5):1977-1982 (1999). Classic quotidian fever was found to be associated with significantly lower levels of plasma IL-6. The published evidence shows that there is a genetically determined difference in the degree of the IL-6 response to stressful stimuli between individuals (Coulthard et al. (Blood) 92(8): 2856-62 (1998)). Thus individuals with genetically linked quotidian fever are likely to be at enhanced risk for a number of drugs that elicit IL-6 expression as part of their inherent toxicity.

The level of expression of the enzyme thiopurine methyltransferase is an important determinant of the metabolism of thiopurines used in the treatment of acute lymphoblastic leukemia and acute myeloid leukemia. TPMT expression displays genetic polymorphism with 10% of individuals having intermediate and one in 300 undetectable levels. Individuals who do not express TPMT are at extreme risk of severe cardiotoxicity when treated with compounds such as azathioprine (Collie-Duguid et al. (Pharmacogenetics) 9(1):37-42 (1999); Coulthard. et al. (Blood) 92(8):2856-62 (1998)). In another example where altered expression of tox-response genes affects the response to specific drugs, experiments have recently demonstrated that overexpression of the human HAP1 protein sensitizes cells to the lethal effect of bioreductive drugs. Prieto-Alamo et al. (Carcinogenesis) 20(3):415-9 (1999).

Altered expression can come from many causes besides mutations in the promoter region. These include, include mutations in the transcription factors or receptors that regulate a gene and gene duplications. While cDNA sequence analysis of a normal sequence that had been duplicated would not detect any change in the coding regions of the genes of interest, gene expression analysis would. For example, two active copies of the X-linked gene spermidine/spermine N1-acetyltransferase (SSAT) in a female lung cancer cell line have been associated with an increase in sensitivity to an anti-tumor polyamine analogue. Mank-Seymour et al. (Clin. Cancer Res.) 4(8): 2003-8 (1998). Duplications in the CYP2D6 or CYP2C19 genes have been shown to be linked with sensitivity to a number of drugs including warfarin, codeine and clofenac. Lundqvist et al. (Gene) 226 (2): 327-38 (1999); Yasar et al. (Biochem. Biophys. Res. Commun.) 254 (3): 628-31 (1999).

There are numerous examples where expression polymorphisms comprise a significant percentage of the population. For example, a genetic polymorphism in the metabolism of the anticonvulsant drug S-mephenytoin has been attributed to defective CYP2C19 alleles. This genetic polymorphism displays large interracial differences with the poor metabolizer (PM) phenotype representing 2-5% of Caucasian and 13-23% of Oriental populations. Ibeanu et al. (J. Pharmacol. Exp. Ther.) 286(3): 1490-5 (1998). Several individuals showing poor metabolic capacity to coumarin and (+)-cis-3,5-dimethyl-2-(3-pyridyl)thiazolidin-4-one hydrochloride show very low levels of the CYP2A6 gene product. See Nunoya et al. (Pharmacogenetics) 8(3):239-49 (1998).

There are multiple additional examples of reported variation in genes known to be important in toxic responses, but clinical investigation has not yet been performed to determine their relative susceptibility to specific drugs. The human UDP-glucuronosyltransferase (UGT1A) locus is regulated in a tissue specific fashion in liver and extrahepatic tissues. Activity assays demonstrated 2- to 4-fold inter-individual differences in UGT activity and qualitative differences between individuals. The polymorphic regulation of UGT1A gene products in gastric tissue may be the biological basis that

determines inter-individual differences in extrahepatic microsomal drug metabolism.

Strassburg et al. (Mol. Pharmacol.) 54(4):647-54 (1998).

Very importantly, it is likely that many mutations in single genes result in altered expression of many more genes, an amplification effect. A knock-out mutant has been  
5 created in mice that destroyed the function of a single gene, the au-beta 6 gene. The resulting animals showed altered basal expression of 101 genes in lung epithelial cells.  
Kaminski et al. (New York Academy of Sciences meeting, Toxicology for the Next Millenium, Airlie VA, USA) September 1999.

Single mutations in any one of hundreds of key toxicity genes can potentially cause  
10 differential basal levels of expression of many additional genes. It may be the altered expression of these genes that render the cell, or organism sensitive to toxic stress, not the initial mutation by itself.

Gene expression analysis has been used to predict who will respond beneficially to the therapeutic effects of treatments. The levels of Bax and Bcl-2 expression after  
15 radiotherapy have been used as prognostic markers in patients with human cervical carcinoma. Harima et al. (J Cancer Res Clin Oncol 124(9): 503-10. (1998). In acute myeloid leukemia, coexpression of at least two proteins, including P-glycoprotein, the multi-drug resistance-related protein, bcl-2, mutant p53, and heat-shock protein 27, have been reported to be predictive of the response to chemotherapy. Kasimir-Bauer et al. (Exp Hematol) 26(12): 1111-7 (1998). The work by Kasimir-Bauer et al. shows that gene expression profiling can be used to predict who will benefit from the therapeutic effects of a drug; it does not address the question as to who will suffer enhanced toxicity of a drug.  
20

All of the above examples show that altered levels of gene expression of a certain set of tox-response genes are associated with qualitatively or quantitatively distinct  
25 responses to the toxic effect of different drugs. Many of the examples show that DNA sequence polymorphisms would not be sufficient to predict hypersensitive individuals. Finally, the disclosure and examples herein show that measurement of a multiple set of tox-

response genes will reveal patterns of gene expression that will identify hypersensitive individuals for specific types of toxicity.

Experimental Identification of Genes

5       Genes associated with hypersensitivity to an agent may be identified in a variety of ways experimentally. Generally the expression of genes that are differentially expressed in total across cell, organ and tissue types in humans, in particular in response to toxic insult is evaluated to determine genes associated with hypersensitivity in an individual. In one embodiment, a method of identifying genes associated with hypersensitivity to an agent is  
10 provided, that comprises comparing the gene expression profile of cells treated with an agent with the gene expression profile of untreated cells, and determining genes in the treated cells that have altered expression due to the treatment, thereby to identify one or more genes associated with hypersensitivity to the agent. The cells may comprise one or more different cell types, wherein each said cell type comprises a gene associated with  
15 hypersensitivity to the agent. Alternately, the cell types are derived from a single tissue or organ.

Exemplary cell types are those derived from a specific organ , cell or tissue, such as kidney, liver, lung, heart, breast, lymphocytes, neuronal cells, skin, or intestine, such as HepG2, Caco-2, MCF-7, Jurkat, Daudi, HL-60, MCL-5, SKBR-3, SKOV-3, PC-3, WISH  
20 and HeLa.

Another method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent comprises comparing the gene expression profile of multiple cell types of an individual known to be hypersensitive to an agent with the gene expression profile of said cell types in an individual known not to be  
25 hypersensitive to the agent; and identifying genes from said multiple cell types having a pattern of differential gene expression, wherein the pattern of differential gene expression is associated with hypersensitivity to the agent.

An alternative to this method comprises, comparing the gene expression profile of multiple cell types of an individual known to be hypersensitive to an agent before treatment with the agent with the gene expression profile of multiple cell types of the hypersensitive individual after treatment with the agent, and identifying genes from the multiple cell types 5 having a pattern of differential gene expression, wherein the pattern of differential gene expression is associated with hypersensitivity to the agent.

When normal or hypersensitive animals, humans or cells are exposed to a selected agent, gene expression changes can be analyzed in genes such as those listed in Table 3, 4, 10 5, 6, 8, 10 and 11. Different types of toxic insult lead to different patterns of gene expression changes in normal, as well as in hypersensitive individuals. Since substantially all compounds elicit toxicity at a high enough dose, the mechanisms of drug toxicity in normal individuals has been well examined. Genes that cells induce to combat the toxic effect of various compounds are important for anti-toxicity for each compound. Patterns of gene expression of these genes in individuals who show hypersensitivity to a given 15 compound that differ from the pattern of differential expression of normal individuals, with or without treatment can be identified. Using these methods, sets of genes that have characteristic expression in hypersensitive individuals that differs from normal individuals may be identified.

Subsets of genes and expression profiles thereof that can be used to identify 20 hypersensitive individuals are identified as follows. A technique such as amplified fragment length polymorphism (AFLP) or serial analysis of gene expression (SAGE), which are known in the art, is used to compare gene expression profiles from treated and untreated human cells. The agent is administered at a toxic dose. This procedure identifies all candidate genes within the cells that respond to the toxic stimuli posed by a particular 25 agent. The method further comprises using a technique, such as AFLP or SAGE, which are known in the art, to compare the gene expression profiles from treated and untreated normal cells. This step would identifies all genes within an individual that respond to that

agent. It also permits investigators to understand the normal expression range of individuals who are not hypersensitive. A technique, such as AFLP or SAGE, is used to compare gene expression profiles for samples from treated and untreated hypersensitive individuals or cell cultures derived therefrom. This step identifies all genes within hypersensitive individuals that respond to the treatment by that agent. It also allows investigators to understand the expression range of hypersensitive individuals. This permits identification of the genes that were differentially expressed in all of the above experiments, thus eliminating genes associated with therapeutically beneficial effects and individual variation in expression of genes unrelated to the compound. The expression of these genes can then be measured in a larger population of normal and hypersensitive individuals using, for example gene arrays, RT-PCR or other techniques known in the art to confirm the correlation between those genes identified in the above procedures and hypersensitivity observed in particular individuals.

Gene expression responses to toxic stimuli can be analyzed using a database of information. The first method is to determine which genes are induced and what is their function. For example, if all genes induced by a compound are regulated by DNA damage, the interpretation is that the compound causes DNA damage. This interpretation requires a database about the function and regulation of all genes in the database. Another method of interpretation is to determine whether the gene expression pattern induced by a second compound is similar to that induced by a compound, the toxicity of which is well-characterized. This approach to interpretation requires an extensive database of gene expression profiles generated from well-characterized compounds. Table 7 shows a partial list of well-characterized compounds for which gene expression data has been generated.

The methods of gene expression analysis discussed herein can be performed using a computer system with computer code suitable for accessing and comparing the gene expression profile determined according to the methods of this invention. Suitable software will also rank the results of these analyses. Computer code suitable for these

purposes can be programmed by a person skilled in the art. Exemplary software and a gene expression profile database related to toxicology are commercially available from Phase-1 Molecular Toxicology, (Santa Fe, NM), for example, Chem Profiler<sup>TM</sup> and Matrix Express<sup>TM</sup>.

5

Examples of Genes Associated with Hypersensitivity

Several drugs have been shown to elicit allergic reactions in a subset of the population. The more extreme form of these allergic reactions can be quite severe and involve extensive damage of significant portions of the skin covering the body. Many 10 patients die from dehydration and infection. The extreme form of these allergic reactions have the names Steven Johnson Syndrome and TEN (Toxic Epidermal Necrosis). Drugs known to elicit Steven Johnson Syndrome and TEN and less severe forms of skin allergy include navirapine, dapsone, acebutolol, trimethoprim, sulfasalazine, sulfacetamide, sulfadiazine, sulfamethoxizole, sulfasoxazole, sulfamethizole cotrimoxazole, amoxicillin, 15 phenytoin, sulfonamide and penicillin.

Gene expression data suggests that the expression levels of a relatively small number of genes can identify who will develop allergic reactions to these drugs. The genes whose expression in CD8 T Cells and keratinocytes is likely to identify hypersensitive individuals include: inducible NOS, Ki-67, Transglutaminase-1, IL-1, FASL, TNF-alpha, 20 CD11b/CD18, p75-R-TNF (TNF Receptor), IL-6 receptor, G-CSF receptor, HSP-70, INF-gamma, ICAM-1, VCAM-1, ECAM-1, and TGF-beta.

While not being limited to any theory, it is believed that there is a similar molecular mechanism for both Steven Johnson Syndrome and TEN. The invention provides a method to determine who will develop these syndromes prior to taking these drugs.

25 All publications, patents, and patent applications referred to herein are incorporated herein by reference.

The following examples are intended to illustrate but not to limit the invention.

EXAMPLES

5

Example 1: Identification of Genes Associated with Hypersensitivity and Screening of Subjects Prior to Drug Administration

Initially, one or more compounds predetermined to cause blood toxicity, such as agranulocytosis, in at least 4% of the patient population, are chosen, e.g. Haldol<sup>TM</sup> (haloperidol). The differential gene expression profile associated with Haldol<sup>TM</sup> (haloperidol) is determined in neutrophils from both normal and hypersensitive subjects when exposed to high concentrations of Haldol<sup>TM</sup> (haloperidol). The gene expression profile from untreated and treated cells is compared using for example, AFLP, a microarray of the genes listed in Tables 3 and 4, or SAGE, to identify genes that vary as a function of toxicity and vary as a function of hypersensitivity to the Haldol<sup>TM</sup> (haloperidol). Next, gene expression from clinical samples from a patient population exposed to Haldol<sup>TM</sup> (haloperidol) or a placebo is measured. The clinical samples are provided by the manufacturer of Haldol<sup>TM</sup> (Hoechst Marion Roussel). Genes are identified that co-varied with the hypersensitivity status. Additional clinical samples are blinded and provided by the manufacturer which includes samples from normal and hypersensitive subjects. Using the present invention, prediction of the hypersensitivity status is based upon gene expression profiles. The level of accuracy of the prediction or correct identification is determined by unblinding the compounds.

In the final stage, gene expression analysis of the key set of genes would be performed on a prospective basis with new patients just beginning treatment with Haldol. The level of accuracy of the prediction or correct identification of hypersensitivity is determined by monitoring patients over time to see if those predicted to develop

agranulocytosis indeed did so. This empirical approach is then be extended to other drugs and other drug manufacturers.

Example 2: cDNA Probe Production

5 A fluorescent dye labeled cDNA probe complementary to the mRNA component of cellular RNA harvested from cells exposed to toxicologic challenge is produced by this protocol, which is designed to produce sufficient Cy3 labeled probe from one experimental sample, and Cy5 labeled probe from one control sample, to develop one microarray slide. The procedure is scalable to easily accommodate, for example, 16 samples. This will  
10 produce sufficient probe mixtures for at least 8 microarray slides. General procedures as described, for example, in Gerard et al. (Focus®) 14:91 (1992); Kotewitz et al. (Gene) 35: 249 (1985); and Gerard et al. (DNA) 5: 271 (1986) are utilized.

cDNA probes may be used in an assay for detecting expression of genes associated with hypersensitivity to an agent. In one embodiment, microarray slides are provided that  
15 contain ssDNA sequences, or targets, from a number of toxicologically relevant genes. The microarray slides, for example, may be 3"x 1" glass microscope slides comprising an array of micron-scale spots of ssDNA sequences on the upper face. The DNA may be bound to the slide using covalent linkage chemistries known in the art.

Total RNA from cells contains mRNA species that are homologous to these  
20 sequences. "Total RNA (high quality)" refers to substantially total cellular RNA. As RNA is very labile, special care must be taken to insure that it is of sufficient integrity at the time of use as template in the production of probe. The level of these mRNA species is proportional to the degree of induction of the gene by the agent under study. This protocol describes the production of fluorescent labeled cDNA probe from the total RNA of cells  
25 which have either been exposed to the agent under study, or are serving as a non-treated control. These probes are then pooled and hybridized to the microarray slide. The experimental and control probes are distinguishable because the Cy3 and Cy5 labels

fluoresce at different wavelengths. The degree to which each probe binds to a specific gene sequence on the slide reveals the level of induction of that gene in the cells exposed to the agent under study.

5      The following materials are used:

	<u>Material</u>	<u>Amount</u>	<u>Exemplary Source</u>
	DEPC treated water	10ml	Ambion®
	Alk Water (pH 7.5 with NaOH)	1ml	
10	Total RNA (of high quality) or Messenger RNA (of high quality)	10µg/sample 2µg/sample	
	First strand buffer	4µl/sample	
	0.1 M DTT	2µl/sample	Sigma®
15	1:8 dilution Cy3 dCTP (3-amino-propargyl-2'-deoxycytidine 5'-triphosphate) (i.e., 0.125mM Cy3 dCTP)	1µl/exp. Sample	Amersham®
	1:10 dilution Cy5 dCTP (3-amino-propargyl-2'-deoxycytidine 5'-triphosphate) (i.e., 0.1mM Cy5 dCTP)	1µl/control sample	Amersham®
20	SuperscriptII (RT)	1µl/sample	Life Technologies, Inc.
	ANTI-RNase	1µl/sample	Ambion®
	7.5 M ammonium acetate	34µl/sample	Sigma®
	70% EtOH	1ml/sample	J. T. Baker®
	95% EtOH	220µl/sample	J. T. Baker®
25	Nucleotide Mix "3"	1µl/exp. sample 0.5 mM dATP/dGTP/dTTP 0.125 mM dCTP	
	Nucleotide Mix "5"	1µl/control sample 0.5 mM dATP/dGTP/dTTP 0.15 mM dCTP	
30	Stock anchored oligo dT:	4µl/sample 0.25µg/µl of each oligo dT (in Water @ -20°C)	
	RNase Zap	(1) bottle The RNA Co.™	
35	Wet ice	(1) bucket	
	Qiagen Qiaquick PCR purification kit	(1) ea Qiagen®	
	PE/ETOH	(1) bottle (100 ml PE buffer + 400 ml >96% EtOH)	
	EB Buffer	10 ml (10 mM Tris-HCl pH 8.5)	

**General Protocol**

Steps are performed at room temperature unless otherwise specified. Work areas are cleaned and swabbed with RNase Zap. Gloves are worn at all times. RNase (RNA specific endo-and exo-nucleases) is a ubiquitous and very stable enzyme. Standard cleaning and/or autoclaving will not remove or inactivate it. Therefore all materials contacting the samples must be known RNase-free. All water, including for buffers, must be DEPC-treated. DEPC treatment consists of an autoclaved solution of 0.1% Diethyl pyrocarbanate in de-ionized water.

Preparation of RNA template in water is implemented by adjusting mRNA to a concentration of 2 $\mu$ g/7 $\mu$ l or total RNA to a concentration of 10 $\mu$ g/7 $\mu$ l for each sample in a standard microfuge tube. If concentration adjustment requires dehydration in the Speedvac™, 1  $\mu$ l Anti-RNase is added prior to dehydration. The reaction solution is prepared by adding 4  $\mu$ l of stock anchored oligo dT per tube, heating at 70°C for 10 minutes in a heat block, spinning 5 seconds in microfuge, and placing on ice for 2 minutes.

15 The following is then added to each tube:

4  $\mu$ l 5x First Strand Buffer for SuperscriptII

2  $\mu$ l 0.1 M DTT

and either (for treated samples):

1  $\mu$ l Nucleotide Mix "3"

20 1  $\mu$ l of 1:8 dilution of Cy3

or (for control samples):

1  $\mu$ l Nucleotide Mix "5"

1  $\mu$ l of 1:10 dilution of Cy5.

25 The tube then is incubated at room temperature for 10 min. The dCTP is added to limit the concentration of Cy dCTPs incorporated. Due to the size of the Cy dCTP, the polymerase will fall off the template if more than two are incorporated in a row.

To perform the reaction, 1  $\mu$ l SuperScriptII is added to each tube, and the contents mixed gently. The tube then is incubated for 1.5-2 hr. at 45°C in a heat block, keeping the reaction protected from light. The fluorescent dyes Cy3 and Cy5 are sensitive to light. Excessive exposure during processing will reduce the intensity of emission upon final scanning.

5 To collect the labeled cDNA probe, ethanol precipitation is implemented by adding to each tube 46 $\mu$ l of water, 34 $\mu$ l of 7.5M ammonium acetate and 220 $\mu$ l of 95% EtOH, and then incubating at -80°C for 15-20 min. If desired, procedure may be interrupted at this point. The sample may be stored at -80°C for up to 7 days.

10 The tubes are loaded in centrifuge with orientation of lid noted, centrifuged for 15 min at 20800 x g, and the supernatant discarded, to obtain a visible pellet (pink for Cy3, blue for Cy5). The pellet is washed by adding 750 $\mu$ l 70% EtOH per tube and vortexing briefly, centrifuging at 20800 x g for 10 min, decanting and discarding the supernatant, centrifuging the pellet and optionally gently removing remaining EtOH with a pipette, 15 while being careful not to loosen the pellets. The pellet is allowed to dry for 10 min. at room temp, but not over drying by using a vacuum, and resuspended in 40 $\mu$ l water. cDNA/mRNA hybrid is denatured by incubating at 95°C for 5 min. in a heat block. The tube then is spun 5 seconds in microfuge.

20 The labeled cDNA probe is purified in an adaptation of the procedure described on page 18 of the QIAquick Spin Handbook, (1997) Qiagen®. To bind the cDNA probe to a column, 200  $\mu$ l of Buffer PB is added to each 40 $\mu$ l probe solution, the QIAquick spin columns are placed in 2 ml collection tubes, and the samples are applied to the QIAquick columns and centrifuged at 10,000 x g for 2 min. The flow-through is discarded and QIAquick columns replaced into the same tubes.

25 To wash bound cDNA probe, 750 $\mu$ l Buffer PE/ETOH is added to each column, and the column incubated for 1 min. at room temp. The column is centrifuged at 10,000 x g for 2 min., and the supernatant discarded. The wash is repeated. QIAquick columns are

placed back in the same tubes, and centrifuged for an additional 1 min at maximum speed with tube lids open. Residual ethanol from Buffer PE will not be completely removed unless the flow-through is discarded before this additional centrifugation.

5 QIAquick columns are placed in clean 1.5ml microfuge tubes. To elute the cDNA probe, 40 $\mu$ l (+/- 10 $\mu$ l) Alk. Water is added to the center of each column. The tubes are incubated for 1 min, centrifuge at 6000 x g for 1 min., and the elution steps repeated once into same tube. The elution buffer is dispensed directly onto the QIAquick membrane for complete elution of bound cDNA.

10 To quantify the cDNA probe, each sample is put in ~80 $\mu$ l of EB buffer, and transferred to one well of a 384 well plate. Scanning, including the measurement and recording of the type and degree of fluorescence from each spot on a processed microarray slide, is accomplished in a confocal laser scanning fluorimeter. The fluorimeter is set to the appropriate excitation/emission frequencies and records the level of emission for the sample. The exposure time and intensity is controlled, because exposure of the label to 15 strong light incrementally reduces its fluorescent activity. Values from this procedure are the result of many variable factors. Therefore it is preferable to compare to an archive of values produced from the same procedure and equipment.

20 To prepare the final probe mixture, the Cy3 labeled experimental probe is combined with the Cy5 labeled control probe. If a control requires multiple reactions, they are combined prior to aliquoting equal amounts to the experimental samples. The combined probes are concentrated to ~1 $\mu$ l in a Speedvac at a temperature not exceeding 45°C. If the probe is not used immediately, 10  $\mu$ l water is added and it is stored at 4°C.

Example 3: Determination Of Gene Expression Changes Associated With Toxicity

25 To determine genes useful for identifying patterns of genes associated with toxicity, animals were exposed to concentrations of selected compounds that elicit peroxisome proliferation, a type of liver toxicity. Treatments were with WY 14,643, gemfibrozil and

clofibrate in Sprague Dawley rats. Each compound was administered in 1% carboxymethylcellulose/0.2% Tween 80 by oral gavage daily for 14 days. Administered doses were to three animals per dose per time point as follows; WY14,643, 40 mg/kg/day; gemfibrozil, 24 mg/kg/day and 100 mg/kg/day, and clofibrate 40 mg/kg/day and 250

5 mg/kg/day.

Gene induction was measured using microarrays consisting of 250 toxicologically relevant rat genes using the hybridization protocol described above. As illustrated in Figure 4, several genes were induced by the treatment, example given is for WY14,643. This figure shows a gene expression profile showing the relative induction levels compared 10 to untreated controls. As shown in Figure 4, the genes referred to in Figure 4 as A (Cytochrome p450 4A *CYP4A*, B (Enoyl Co-A Hydratase), C (3-ketoacyl CoA thiolase 2), D (Acyl CoA Oxidase), and E (Ketoacyl CoA thiolase type 1), had enhanced expression in comparison to the control after treatment with the compound. These genes were found to be induced by a variety of other peroxisome proliferating agents including gemfibrozil, 15 clofibrate, fenofibrate and DEHP. This set of genes was thus empirically shown to be induced by a variety of compounds that exhibit a specific type of hepatotoxicity, peroxisome proliferation. By way of example, individuals who display hypersensitivity to these types of compounds should show altered expression of this set of genes.

20 Example 4: Probe For Hepatocyte Growth Factor

New genes associated with and predictive of toxicity were identified. Different types of damage to the liver cause the formation of dead and dying hepatocytes, which the liver replaces to maintain its function. Induction of the hepatocyte growth factor receptor gene by toxic stimuli in both rats and humans was examined. When several nitrosoureas 25 including streptozotocin, carmustine and MNU were used to determine gene expression profiles, all of these compounds induced several genes in common. These compounds are all known to form covalent adducts to the DNA in liver and liver cells. All compounds, for

example induce both the hepatocyte growth factor receptor gene and the glutathione transferase gene. Exemplary data is provided in Figure 1 which shows the gene expression profile in the liver of male Sprague-Dawley rats when treated with the hepatotoxicant streptozotocin.

5       The probe for the hepatocyte growth factor receptor gene was created by cloning at least a 250 base-pair section from the 3' coding region of the gene starting with total genomic DNA. The fragment was derived by PCR from genomic DNA using two primer with appropriate linkers for insertion into a plasmid vector. A single stranded probe complementary to the cDNA sequence was attached to a glass slide array using a  
10 polyamine attachment.

In more detail, an example of creation of a specific probe for the hepatocyte growth factor receptor is as follows. The first step in the process is obtaining the sequence for the gene. The search for gene sequence, either by gene name or accession number, is performed using the NIH National Center for Biotechnology Information website using  
15 Genbank ([http://www2.ncbi.nlm.nih.gov/genbank/query\\_form.html](http://www2.ncbi.nlm.nih.gov/genbank/query_form.html)). The accession number for the rat hepatocyte growth factor receptor gene is X96786. When the sequence of interest is located, the sequence information is copied to a Microsoft Word file. Intron sequences are then removed, if present, as well as numbers and white spaces. The resulting condensed sequence is then submitted to a PCR primer design software program, such as  
20 Primer3 (<http://www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>). Primers are selected that optimally have a  $T_m$  in the range of 60°-63°C. The optimal length of the gene fragment is 500 bp. Shorter fragments are chosen if the starting sequence is shorter than 500 bp.  
Once the primers are designed, the sequence that is flanked by the primers is submitted to a BLAST search. BLAST (Altschul et al (Nucleic Acid Res) 25: 3389-3402. (1997)) is a  
25 sequence analysis software program supported by the NIH. The BLAST search software searches for other DNA sequences that are homologous to the target sequence and ranks these sequences according to the amount of homology. This ensures that the chosen gene

fragment sequence will not cross-hybridize with a gene sequence other than the desired sequence. PCR primers are ordered and an attempt is made to isolate the gene fragment from a cDNA library that is created by reverse transcription of RNA from either a cell line(H4IIE) or rat tissue. Upon identification of a PCR band of the correct size, the PCR  
5 product is cloned into a vector (TA cloning vector, Invitrogen Corp., Carlsbad, CA). Following cloning, a bacterial mini-prep is performed to amplify and isolate the plasmid containing the gene fragment of interest. The region of the plasmid containing the gene fragment is then sequenced. If this sequence matches the original target sequence, the target sequence of this clone is amplified by PCR, purified (Wizard system, Promega  
10 Corp., Madison, WI), quantified, and used for spotting.

The probe refers to a population of cDNAs bearing fluorescently active ligands which are produced from the mRNA of the cells under examination, while "probe mixture" refers to a mixture of two or more populations of cDNA. The cDNAs may also be labeled with a variety of ligands, such as fluorescently active ligands, radioisotope ligands or  
15 biotinylated ligands.

#### Example 5: Glutathione Transferase Positive Foci

Enhanced gene expression and co-induction of genes associated with the formation  
20 glutathione transferase positive foci was identified.

Certain types of toxic liver damage produce glutathione transferase positive foci  
Lemmer et al. (Carcinogenesis) 20:817-824 (1999) which are cells that are in the late stages  
of dying. In response, neighboring hepatocytes must replicate in order to replace the dying  
cells and induce expression of hepatocyte growth factor so that they are 'primed' for  
25 growth hormone signals.

Co-induction of the glutathione transferase and hepatocyte growth factor receptor genes was determined by hybridization to microarrays containing at least 300 human toxicologically relevant genes using the hybridization protocols described above.

Figure 2 is a graph showing the results, which indicated a very strong correlation between the induction of the glutathione transferase and hepatocyte growth factor receptor genes. Co-induction thus shows correlation to focal cell death occurring in the liver.

Example 6: Heart Muscle Tissue Gene Expression Profile

Animals were exposed to doxorubicin, a cardiotoxin. Male Sprague-Dawley rats were treated with 1 mg/kg doxorubicin in 5% saline for 6 ho 24 hours, and 7 days and 6 weeks with one dose per day and a 6 week recovery period. A gene expression profile of heart muscle tissue cells was then obtained. RNA was isolated and the gene expression profile was analyzed as described below. Gene expression of all genes listed in Table 8 was determined. The results of the gene expression of the first 66 genes is shown in Figure 3.

As can be seen from Figure 3 and Table 8, several genes, including activating transcription factor 4, activin receptor type II, ataxia telangiectasia, c-jun, carnatine palmitoyl-CoA transferase, DNA Dependent helicase, Epozide hydrolase, farnesol receptor, Gadd 45, Interleukin 6, MDM-2, Ribonucleotide reductase subunit M1 and at least 10 others were differentially expressed at significant levels. Many of these genes, including Carnatine Palmitoyl transferase, Epoxide hydrolase, Farnesol receptor, Lipoprotein lipase precursor, and MDM-2 have never been reported or previously known to be induced by cardiotoxicity.

Thus a profile of gene expression characteristic of the cardiotoxin, doxorubicin was obtained. Genes thus identified as having altered expression in the presence of cardiotoxin are significant, because individuals with diminished or altered expression of the induced genes may potentially be hypersensitive to the toxicity of doxorubicin. Such

hypersensitivity could manifest itself at the molecular level as altered induction of these genes as well as a shift in the dose-response curve such that the same genes would be induced at lower concentrations.

5      Example 7 Determining genes associated with hypersensitive reaction to penicillin

Three different methods, differential display, microarray technology, and Taqman® assay were used to determine genes associated with hypersensitive reaction to penicillin. Seven self-described penicillin-sensitive individuals and six individuals self-described to have normal reaction to penicillin were tested by differential display. Six self-described 10 penicillin-sensitive individuals and six individuals self-described to have normal reaction to penicillin were tested by microarray technology.

15      1. Lymphocyte culture

Six individuals self-described as penicillin sensitive and seven individuals self-described as having normal reaction to penicillin were used to determine potential hypersensitive reactions to penicillin in humans. Peripheral blood leukocytes (PBL) were isolated from a population of individuals, cultured with PHA at a standard concentration for culturing lymphocytes for 24 hours, washed, cultured for another 24 hours without 20 PHA, and divided into two groups. One group was exposed to penicillin *in vitro* for 24 hours and the other group was not exposed to penicillin as a control group. At a non-toxic dose of 1250 µg/ml, penicillin G is known to elicit an immune response in peripheral blood of individuals with proven penicillin G allergy.

25      2. Isolation of RNA from cultured lymphocytes

RNA from select individual from both groups (treated and untreated) of cultured lymphocytes was isolated as follows. Total RNA of high quality and high purity is isolated from cultured cells by using Qiagen QIAamp® RNA blood mini kit and 2-

mercaptoethanol. RNA degradation by RNases is not desirable when synthesizing fluorescent cDNA for hybridization with the penicillin array. Precautions are taken to minimize the risk of RNA degradation by RNases by wearing gloves, treating work areas and equipment with a RNase inhibitor, for example, RNase Zap (Ambion® Products, 5 Austin, TX) and keeping samples on ice. This total RNA isolation technique is based on a Qiagen QIAamp®RNA blood mini kit and is used with some modification for human lymphocyte cells in a T-75 flask.

Cells are checked under the microscope to make sure that they are viable. Cells are dosed with penicillin on the third day in culture (48 hours after introduction of the cells into 10 culture).

Cells are scraped from the flask and poured into a 50 ml conical tube. The flask is then rinsed with 10 ml of room temperature PBS. The PBS wash is removed with a pipette. The tube is then spun for 10 minutes at 1,000 rpm and the supernatant pipeted off. The remaining pellet is resuspended in 600 $\mu$ l of freshly prepared RLT buffer (RLT buffer 15 requires the addition of 10 $\mu$ l of beta mercaptoethanol for each 1.0 ml RLT) by vortexing. The resuspended pellet is pipeted into a QIAshredder® column and centrifuged for 2 minutes at 14,000 rpm in a Eppendorf® 5417C centrifuge. The QIAshredder® column is discarded and 600  $\mu$ l of 70% ethanol added to the lysate. The lysate is then pipeted into a QIAamp® spin column sitting in a 2 ml collection tube and centrifuged for 15 seconds at 20 14,000 rpm. Any remaining lysate is placed on the same column and the centrifugation is repeated. The QIAamp® spin column with the RNA bound to the column is transferred to a new 2 ml collection tube. 700 $\mu$ l of Qiagen® RW1 buffer is added to wash the column and centrifuged for 15 seconds at 14,000 rpm. The QIAamp® spin column is transferred to a new 2 ml collection tube. 500 $\mu$ l of Qiagen® RPE buffer is added to the column and 25 centrifuged for 15 seconds at 14,000 rpm. The QIAamp® spin column is transferred to a new 2 ml collection tube. 500 $\mu$ l of Qiagen® RPE buffer is added to the column and centrifuged for 3 minutes at 14,000 rpm. The QIAamp® spin column is transferred to a

new 2 ml collection tube and centrifuged for 1 minute at 14,000 rpm. The QIAamp® column is transferred to 1.5 ml microcentrifuge tube and 50 µl of RNase-free water is added to the column and centrifuged for 1 minute at 14,000 rpm. An additional 50 µl of RNase-free water is added to the column and centrifuged for another 1 minute at 14,000  
5 rpm.

To measure the yield, the O.D. reading is taken at 260nm on a Beckman DU®350 UV vis spectrophotometer. 1.0 µl RNA is added to 49 µl of sterile nanopure water and the O.D. reading is taken and calculated as follows:

$$(\text{Absorbance}) \times (\text{dilution factor}) \times (40)/1000 = \text{amount of RNA in } \mu\text{g}/\mu\text{l}$$

10 Example: absorbance = 0.45

Dilution factor = 50

$$\frac{(0.45) \times 50 \times 40}{1000} = \text{RNA concentration in } \mu\text{g}/\mu\text{l}$$

1000

The sample is stored in -80°C freezer.

15

### 3. MessageClean® of Total RNA

It is important that total RNA that is used to make mRNA differential display is absolutely free of DNA contamination. Regardless of the method used for RNA isolation, a cleaning step is important to ensure the removal of DNA contamination, especially if the  
20 differential display banding pattern on the denaturing polyacrylamide gel is independent of the reverse transcription step. MessageClean® from GenHunter (Nashville, TN) was used to clean total RNA. Components for twenty RNA sample cleanings included the following materials: 140 µl 10x Reaction Buffer, 20 µl GH-DNase I (RNase free, 10 units/µl), 140 µl 3M NaOAc, and 1 mL DEPC-treated H<sub>2</sub>O. For DNase I digestion, the following materials  
25 were added in order: 50 µl total RNA (10-50 µg), 5.7 µl 10x Reaction Buffer, 1 µl DNase I (10 units/µl) for a total volume of 56.7 µl. The materials were mixed well and incubated at 37 degrees for 30 minutes. A 3:1 phenol/chloroform mixture is used to ensure removal of

protein contamination and DNase I from the RNA. About 40  $\mu$ l of phenol/chloroform is added to the mixture, vortexed for 30 seconds, and allowed to sit on ice for about 10 minutes. Then the mixture was spun in an Eppendorf centrifuge at 4 degrees for 5 minutes at maximum speed and the upper phase of the mixture is collected. Ethanol precipitations was performed as follows. About 5  $\mu$ l of 3M NaOAc and 200  $\mu$ l of 100% ethanol was added to the upper phase that was collected. This was placed at -80 degrees for more than 1 hour and then spun for 10 minutes at 4 degrees. The supernatant was removed, the RNA pellet was washed with 0.5 mL of 70% ethanol (in DEPC-treated water), and spun for 5 minutes to remove the ethanol. The tube containing the materials were spun again and the residual liquid was removed. The RNA was re-dissolved in 10-20  $\mu$ l DEPC-treated water. The RNA was quantitated by reading on a spectrophotometer at OD<sub>260</sub>. RNA that is diluted for any purpose, such as quantitation, should not be re-used after freezing and thawing. The integrity of the RNA can be checked by running a few micrograms on a 7% formaldehyde agarose gel and looking for the clear appearance of 28S and 18S rRNA bands.

#### 4. Reverse transcription

In a tube, the following ingredients are added: 9.4  $\mu$ l dH<sub>2</sub>O, 4.0  $\mu$ l 5x RT buffer, 1.6  $\mu$ l dNTP (250  $\mu$ M), 2.0  $\mu$ l of 0.1  $\mu$ g/ $\mu$ l freshly diluted total RNA that is DNase-free, 2.0  $\mu$ l 20 H-T<sub>11</sub>M (2  $\mu$ M) for a total volume of 19  $\mu$ l. The ingredients are mixed well and incubated at 65°C for 5 minutes, 37°C for 60 minutes, 75°C for 5 minutes, and held at 4°C. After the tubes had been at 37°C for 10 minutes, and 1  $\mu$ l of SuperScript II reverse transcriptase (Life Technologies Inc.) is added to each reaction, and quickly mixed by finger tapping the tubes before the incubation continued. At the end of the reverse transcription, the tubes are spun briefly to collect condensation. The tubes are set on ice for PCR or stored at -20°C for later use.

5. PCR to amplify gel band

The following is an exemplary protocol for PCR. The following ingredients are used: 10 µl dH<sub>2</sub>O, 2 µl 10x PCR buffer, 1.6 µl DNTP (25 µm), 2 µl of 2 µm H-AP primer, 2 µl of 2 µm H-T<sub>11</sub>M, 2 µl RT-mix described above (must contain the same H-T<sub>11</sub>M used for PCR), 0.2 µl α-<sup>33</sup>p DATP (2000 ci/mmole), 0.2 µl TAQ DNA polymerase from PE Biosystems for a total volume of 20 µl. The tube containing all these ingredients are mixed well by pipeting up and down and placed in a thermocycler at 95°C for 5 minutes and then amplified for 40 cycles under the conditions of 94°C for 30 seconds, 40°C for 2 minutes, 72°C for 30 seconds and finally held at 4°C until the samples are removed from the thermocycler.

6. Gel electrophoresis

RNA was analyzed by gel electrophoresis to identify possible candidate genes. A 6% denaturing polyacrylamide gel in TBE is prepared and allowed to polymerize for at least 2 hours before using. Then the gel is run for about 30 minutes before any samples are loaded. It is important for all the sample wells in the gel to be flushed and cleared of all urea prior to loading any samples in the wells. About 3.5 µl of each sample is mixed with 2 µl of loading dye and incubated at 80°C for 2 minutes immediately before loading onto the 6% gel. In this example, the loading dye is xylene and after the gel is loaded with the samples obtained from the rounds of PCR, the gel is run at 60 watts of constant power until the xylene dye is about 6 inches from the bottom of the gel. Once the power is turned off, the gel is blotted onto a large sheet of exposed autoradiograph film. The gel is covered with plastic wrap and under dark conditions, the gel is placed in a large autoradiograph cassette with a new sheet of unexposed film, marked for orientation, and the film is allowed to be exposed to the gel at -80°C. The exposure period can be anywhere from overnight to 72 hours. Once the film has been developed, bands of interest, which show differential expression between penicillin sensitive and normal individuals, are identified by alignment

with the developed film and subsequently isolated by cutting the band of interest out of the polyacrylamide gel with a clean scalpel blade. The isolated band is placed in 100 µl of water and boiled at 95% for 5 minutes.

5      7. Cloning re-amplified PCR products for differential display

The following procedure was used to clone re-amplified PCR products from differential display. Material which may be used include the PCR-TRAP® Cloning System (GenHunter®). For a 20ul Ligation reaction, add in order: 10ul dH2O; 2ul 10X ligase buffer; 2ul Insert-ready PCR-TRAP® Vector; 5ul PCR product; 1ul T4 DNA ligase.

10     The reaction is mixed well by finger tipping and is briefly spun. Then the reaction is ligated overnight at 16°C. The reaction can then be used directly for transformation or stored at -20°C. For transformation, the GH-competent cells are thawed in ice water slush for 15 minutes. While the cells are melting, the appropriate number of 1.5ml microfuge tubes are labeled and set on ice. The cells are quickly mixed by finger tipping and are

15     divided into 100ul aliquots into each 1.5ml microfuge tube. The remaining competent cells are immediately re-frozen for future use. The ligation tubes are spun briefly to collect condensation. About 10ul of each ligation mix is added to an above tube containing the competent cells and mixed well by finger tipping and incubated on ice for 2 minutes.

20     About 0.4ml of LB medium is added and the cells are incubated at 37°C for 1 hour. It is important that no Tetracycline be in the LB during this step because the bacteria with recombinant plasmids need time to express the Tetracycline resistance gene. It is recommended that the LB-Tet plates are warmed at 37°C for 1 hour before plating. After vortexing briefly, about 200ul of cells are plated on an LB-Tet plate (containing 10ug/ml of tetracycline). For the lacZ control insert, about 200ul of cells are added to the plate. Then

25     30ul of X-gal is added to the middle of the cells and the cells are immediately spread onto the LB-Tet plate. Unplated cells can be stored at 4°C if replating is needed within 1 week. Once the plate surface is dry, the plate is incubated upside-down overnight at 37°C. The

Tet colonies are scored and the plate is save upside-down at 4°C. Three individual Tet resistant colonies are picked for each clone with a 10ul pipette tip, placed in labeled sterile culture tube containing 3ml of LB broth and grown overnight at 37°C.

5      8. Screening colonies for inserts

Plasmid DNA was isolated using the Qiagen Qiaprep Miniprep kit. PCR was used to check for inserts in the plasmids. For each colony the following PCR reaction mixture was set up:

	dH2O	10µl
10	10xPCR buffer	2µl
	dNTPs (250µM)	1.6µl
	Left primer	2µl
	Right primer	2µl
	Plasmid DNA	2µl
15	Taq DNA Polymerase	0.2µl

The PCR parameters were 94°C for 30 sec, 52°C for 40 sec, 72°C for 1 min for 30 cycles followed by 5 min extension at 72°C and a final incubation at 4°C. All 20µl of the PCR product was analyzed on a 1.5% agarose gel with ethidium bromide staining.

20      Once the positive colonies were identified, they were sequenced by standard methods well-known to a skilled artisan. The sequences were compared to known sequences to determine if the sequence was already known.

As indicated at the beginning of Example 7, either differential display or microarray techniques were used to further determine genes related to penicillin hypersensitivity.

25

9. Genes Identified

By gel electrophoresis, about 260 candidate genes were identified and about 220 were cloned and sequenced to identify genes that predict hypersensitivity to penicillin. A summary of the genes associated with penicillin hypersensitivity is summarized in Table 10. Several new genes were identified that did not match any sequence listing in GenBank.

5 Novel sequences which did not match any BLAST searches or GenBank searches are indicated in Table 10 under the "Identification" column as "no significant match to anything". Thus, provided herein are nucleic acids comprising said novel sequences and fragments thereof as well as amino acid sequences encoded therefrom and fragments thereof. Also provided are nucleic acids that hybridize to said novel sequences under

10 stringent conditions. Such stringent conditions include conditions of a hybridization reaction that allow nucleic acid duplexes to be distinguished based on their degree of mismatch. Means for adjusting the stringency of a hybridization reaction are well-known to those of skill in the art. See, for example, Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, Second Edition, Cold Spring Harbor Laboratory Press, 1989;

15 Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1996 and periodic updates; and Hames *et al.*, NUCLEIC ACID HYBRIDIZATION: A PRACTICAL APPROACH, IRL Press, Ltd., 1985. In general, conditions that increase stringency (*i.e.*, select for the formation of more closely-matched duplexes) include higher temperature, lower ionic strength and absence of solvents; lower stringency is favored by lower

20 temperature, higher ionic strength, and higher concentrations of solvents (for example, formamide or dimethyl sulfoxide).

The following are some of the genes identified using the methods disclosed herein (GenBank identification numbers in parenthesis): hypothetical protein (HSPC004), UBA3 (UBA3) mRNA, clone CTA-732E4 on chromosome 22q12.1, ribosomal protein S7 (RPS7),  
25 myosin-binding protein C, cardiac (MYBPC3), CGI-51 protein mRNA, latexin mRNA, NADH oxidoreductase subunit MWFE, jun B proto-oncogene (JUNB), KIAA0787 protein, fatty acid synthase, polymerase (RNA) II (DNA directed) polypeptide B (140 kD), UbA52

gene coding for ubiquitin-52 amino acid fusion protein, small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) (SNRP70), isocitrate dehydrogenase 3 (NAD<sup>+</sup>) gamma (IDH3G), clone 565E6 on chromosome 11q12-1q22.2, hypothetical protein FLJ20436 (FLJ20436), c-Cbl-interacting protein L7a (RPL7A), ribosomal protein L7a (RPL7A),  
5 ribosomal protein S21 (RPS21), sorting nexin 6 (SNX6), TNF-inducible protein CG12-1 (CG12-1), BRCA2 gene region chromosome 13q12-13, CGI-128 protein mRNA, Tu translation elongation factor, mitochondrial (TUFM), KIAA0787 protein, ribosomal protein L13 (RPL13), ribosomal protein L19 (RPL19), clone 245M18 on chromosome 6p21.32-22.3, clone TCBA00781, chromosome 19 cosmid R26529, tumor suppressing  
10 subtransferable candidate 1 (TSSC1), transferrin receptor (TFRC), ubiquitin-conjugating enzyme E2D 3 (UBE2D3), putative DNA-directed RNA polymerase III C11 subunit, myosin-binding protein C (cardiac) (MYBPC3), tapasin (NGS-17), CoREST protein (COREST) (KIAA0071 protein), dynamin (dynactin complex 50 kD subunit) (DCTN-50), alpla-L-fucosidase, metallothionein-IG (MT1G), Familial Cylindromatosis cyld gene,  
15 cDNA FLJ10589 fis (clone NT2RP2004389), eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), chromosome 16 BAC clone CIT987SK-A-67A1, proteasome (prosome, macropain) subunit beta type 8 (large multifunctional protease 7) (PSMB8), and lectin galactoside-binding soluble 9 (galectin 9). An unexpected result that was found was that there were apparently no p450 genes or  
20 metabolism genes that were gene candidates for penicillin hypersensitivity.

#### 10. Gene Correlations

Gene expression profiles comprised of 180 genes on the penicillin array were compared for similarity between six penicillin-normal individuals and six self-identified penicillin-  
25 sensitive individuals. Three of the penicillin-sensitive profiles were repeat samples taken at different times. As shown in Figure 6, Samples 6005, 6015, and 6042 are from one individual, and samples 6041 and 6043 are from another individual. Using all genes for

comparison, sensitive individuals tend to resemble one another while non-sensitive individuals have little discernable pattern. The one exception is non-sensitive individual 6002, whose profile has some resemblance to the sensitive individuals.

In an exploratory analysis, independent-samples t-tests were performed to suggest which 5 genes were differentially expressed between penicillin-sensitive and penicillin-insensitive individuals. Twenty genes in which the p-value of the t-test showed a statistically significant difference between the two classes at a level of 0.005 or less were identified as indicated in Table 11. Using the 20 genes identified as "discriminator" genes, the correlation between normal individuals and the discriminator genes were calculated as well 10 as the correlation between sensitive individuals and the discriminator genes. The discriminator correlations are shown in Figure 7. Using the 20 discriminator genes and relevance network grouping, a similar correlation resulted. At a 0.9 correlation level, the only group that reveals itself is among the sensitive individuals. At a lower similarity level of 0.8, non-sensitive individual #2, who appeared to be borderline hypersensitive, joins the 15 group of sensitive individuals. Methods of analyzing expression data statistically which are known in the art may be used, such as those described in "Family-Wise Error Rate", Glass, G. and Hopkins, K., Statistical Methods in Education and Psychology (1984), Prentice-Hall; and "Relevance Networks", Butte, A. J. and Kohane, I. S. (2000), Mutual Information Relevance Networks: Functional Genomic Clustering Using Pairwise Entropy 20 Measurements. PSB00, 5:415-426.

Figure 8 shows that the 20 discriminator genes were analyzed for co-regulation, revealing several co-varying groups, as shown in both the similarity matrix and the relevance network grouping.

25 10. Preparation of penicillin arrays

In addition to differential display, microarray techniques were utilized to determine genes related to penicillin hypersensitivity. The following are methods that were used to

prepare microarray for testing for penicillin hypersensitivity. Of 260 potential gel band, 220 were cloned and sequenced. About 180 genes were put on a penicillin array, made as described below, and 20 discriminator genes (Table 11) were selected related to penicillin hypersensitivity.

5

#### Large Scale PCR (in 96-well plates)

For 1000 PCR reactions, 4X Master Mix can be made with the following materials:

10X PCR buffer	10 ml
dATP	200ul (100mM)
dGTP	200ul (100mM)
dCTP	200ul (100mM)
15 dTTP	200ul (100mM)
Amine-linked vector primer (= "3X")	900ul (Forward or Reverse) 1ug/ml
Taq Polymerase	1 ml 5U/ml
H <sub>2</sub> O	<u>12.3 ml</u> <u>25 ml total</u>

20

About 2.5ml aliquots are put into 15ml conical tubes and store at -20°C. One tube is enough for 1 96-well plate of PCR. Alternatively, about 12.5ml aliquots can be used in 50ml conical tubes, which is enough for 5 plates of PCR. dNTPs was obtained from Pharmacia Ultrapure dNTP set, cat#27-2035-02 (set contains all 4, 1ml each) and Taq Polymerase was obtained from Perkin Elmer N808-0155 (comes with 10X buffer). Template and gene-specific primer mix was made for 2 rows, or 16 wells by utilizing the following materials: 400ul H<sub>2</sub>O, 2.5ul plasmid, 15ul of 1ug/ml gene specific primer.

25

To perform PCR, the following steps were performed:

30

1. Take one tube of PCR master mix and add 2 volumes of water (i.e., add 5ml water to 2.5ml MM).
2. Using a multichannel pipette, distribute 75ul MM to each well of a 96-well plate.
3. Add 25ul H<sub>2</sub>O to 2 wells of the plate to serve as negative controls.
4. Add 25ul template and gene-specific primer mix to appropriate wells.

5. Seal all wells with strip caps.
6. Plates can be stored at 4°C for up to 48 hours (maybe more) before cycling.
7. Run PCR using program TKB (95° for 5min, 95° for 15s, 50° for 30s, 72° for 30s, go to step of 95° for 15s and repeat 34 times, 72° for 10min., 4° until PCR needed for subsequent steps
- 5
8. Run product on 1.5% agarose gel and check insert size. (Only need to check 1 well of each "gene.")
9. Clean PCR products using any commercially available kit for cleaning PCR products.

10

#### Gene purification

The ArrayIt™ kit from TeleChem, International, Inc. Sunnyvale, CA was used for gene purification. The following protocol was used:

1. Position a SuperFilter 100 on a 96-well vacuum manifold. Make sure the SuperFilter is  
15 properly fitted to allow a tight seal for vacuum filtration.
2. Add 500 µl of ArrayIt™ Binding Buffer to each well of the SuperFilter 100 using a 12-channel pipetting device set for 500 µl. Pipetting should be performed as quickly as possible (within 1 minute per plate) to minimize the loss of the Binding Buffer due to gravity flow. Avoid splashing the contents from well to well.
- 20 3. Quickly add 100 µl per well of PCR sample for a 96-well plate to the corresponding well of the SuperFilter 100. Transfer the PCR samples to the SuperFilter 100 as quickly as possible (within 1 minute per plate) to minimize the loss of the Binding Buffer due to gravity flow.
4. Immediately mix the Binding Buffer and the PCR sample thoroughly by pipetting up and  
25 down 10 times with an automatic pipetting device. Mixing should be completed as quickly as possible (within 5 minutes after adding the Binding Buffer to the SuperFilter

- 100) to minimize the loss of the Binding Buffer due to gravity flow. void splashing the contents from well to well.
5. Apply a gentle vacuum such that a little trickle flows from the SuperFilter 100 to allowing binding of the PCR product to the SuperFilter 100 membrane. Primers, nucleotides, single-stranded products, salts, and other impurities pass through the SuperFilter 100 into the waste reservoir at the bottom of the vacuum filtration block.
- 10 6. Shut off the vacuum and add 800 µl of Wash Buffer to eachwell of the SuperFilter 100 with a 12-channel pipetting device. Apply a gentle vacuum until all of the Wash Buffer has passed through the SuperFilter 100 membrane. The 800 µl of Wash Buffer used in the first wash step is necessary to remove Binding Buffer and PCR sample that adheres to the walls of the SuperFilter 100 during mixing.
- 15 7. Shut off the vacuum and add 100 µl per well of Wash Buffer to the SuperFilter 100 with a 12-channel pipetting device. Apply a gentle vacuum until all of the Wash Buffer has passed through the membrane. Repeat this step with an additional 100 µl of Wash Buffer. The second and third wash steps remove additional trace contaminants from the bound PCR Product.
8. Apply a full vacuum for 3 minutes to dry the SuperFilter membrane. This removes small amounts of Wash Buffer that may interfere with the elution step and assists in fixing the DNA to the filter prior to elution.
- 20 9. Remove the SuperFilter 100 from the vacuum manifold and place it on an unmarked 96-well microplate.
10. Centrifuge the two plates for 5 minutes at ambient temperature in a microplate centrifuge (~500xg) to remove trace amounts of Wash Buffer. This step aids in eluting the DNA from the SuperFilter and improves yield.
- 25 11. Discard the unmarked microplate containing the residual wash Buffer.
12. Transfer the SuperFilter 100 containing the bound PCR product onto a marked 96-well microplate.

13. Re-hydrate the ArrayIt™ SuperFilter by adding 75 µl per well of H<sub>2</sub>O (ph=8.0) with an automatic pipetting device. For maximal DNA recovery, be sure to add the 0.1X TE directly onto the surface of the SuperFilter membrane. The mild elution buffer (1mM TrisCl, 0.1 mM EDTA) is used to minimize the interference of the buffer in downstream applications.

5

Attaching hypersensitivity relevant genes to glass slide

The genes to be attached to the glass slides are amplified as provided herein. An important modification to the amplification process is the inclusion of amine primers, which can be obtained from any commercial source, i.e. Synthegen, such that a reactive amine group, a derivative thereof, or another reactive group is included in the amplified product. The amplified product is purified by any number of methods disclosed herein and immobilized or "spotted" onto a solid substrate, such as a glass slide, which can react with the amine group on the amplified product and form a covalent linkage.

10

An MD Generation II Array Spotter main instrument (Molecular Dynamics, 928 East Arques Avenue, Sunnyvale CA 04-86-4520) was used for spotting the hypersensitive genes according to following parameters:

MD ARRAY SPOTTER OPERATION

20

The terminology and equipment used in this example comprised the following:

Spotter: MD Generation II Array Spotter main instrument

Spotting Chamber: Area of spotter enclosed in glass which houses the pins, plates, trays and most spotter machinery.

Controller: Dedicated Dell Computer and Monitor to right of Spotter Unit

Pins: (6) fine tubes in the Spotter Unit which pick-up and spot the Target

Slides: Std. size glass microscope slides with a special coating on one side

Plates: Plastic 96 well plates which hold the Target solution to be spotted

Target: A solution of PCR product which the spotter deposits on the slides.

N2 Tank: 5 ft. high steel gas tank labeled "Nitrogen, Compressed"

25

N2 : The N2 gas from the N2 tank

Air Conditioner: Kenmore air conditioner installed in window of spotting chamber

Humidifier 1: Essick 2000 Evaporative Cooler against the window

Humidifier 2:	Bemis Airflow with white flexible duck into the Spotter Unit
Humidifier 3:	Bemis Airflow against the wall
Humidifier 4:	Kenmore QuietComfort 7
Vacuum Pump:	Gast Laboratory Oilless Piston Vacuum Pump
Dampbox:	The plastic sealable container containing an NaCl / water slurry

Materials used for reagent solutions are: Nanopure water, 0.2 M KCl (1/10 dilution of Stock 2M KCL in water), and 95% EtOH Reagent. The temperature control is adjusted to 60°. The spotter chambers are adjusted to be greater than 39 % relative humidity and less than 65° C. The spotting pins are pre-washed for 20 cycles.

#### Slide Preparation/Loading:

When the pre-wash is completed, the slides are first each blown with N<sub>2</sub> gas for about 2 seconds per side. The slides are inserted into the Spotter following Array Spotter Run Values. The slides are aligned using a clean narrow rod orienting it on the center right edge of the slide and gently pushed to the left until the slide is aligned vertically against the metal pins. After slides are loaded and straightened, a visual check is done to make sure no more debris had fallen. The humidity is confirmed to be greater than 39% relative humidity. The MD spotter recognizes 16 plates as a maximum for a run and will pause automatically after 8 plates. The MD spotter also advances sequentially to plates in an invariable order and is not programmable to accommodate unique plate sourcing scheme. Therefore, it is important to manually rotate (or shuffle) plates to accomplish the spotting for the canine arrays.

## 25 Blocking (Slide Preparation post-spotting)

This blocking procedure is important because it reduces the non-specific background signals. The amounts provided in this protocol are for 19 slides, however, a skilled artisan may make modifications accordingly. More staining dishes and slide racks will be required if more than 19 slides are to be blocked. A clean glass container is obtained

and filled with Nanopure H<sub>2</sub>O. The container is placed on a hot plate and heated to a high temperature. A blocking solution is made by adding 2.5 ml of 20% SDS to 500mL blocking solution bottle. The blocking solution is warmed in microwave for 2.5 minutes and checked to determine if the temperature had reached 50°C. If the temperature of the  
5 solution is not at yet 50°C, then the solution is warmed in the microwave at 10 second intervals until it reached the desired temperature. One staining dish is placed on an orbital shaker with 4x SSC solution and turned to an agitation speed of 75 rpm. Slides are placed in metal racks and placed in boiling water for several minutes (i.e. 2 minutes). The slides are taken out of boiling water and allowed to cool briefly. The slides are then transferred to  
10 staining container containing 4x SSC solution on orbital shaker for several minutes (i.e. 2 minutes), rinsed with nanopure water in a staining container, and then briefly placed in blocking solution for about 15 minutes. After 15 minutes, the slides are taken out of the blocking solution and rinsed three times by dipping into three separate containers with nanopure water each time. The tops of the slides are dabbed lightly with a tissue and the  
15 slides are placed in a centrifuge for about 5 minutes at a speed of 1000 rpm.

#### Microarray RT Reaction

An exemplary procedure for labeling the probes is as follows. Fluorescence-labeled first strand cDNA probe is made from total or mRNA by first isolating RNA from control  
20 and treated cells, disclosed *supra*. This probe is hybridized to microarray slides spotted with DNA specific for hypersensitivity relevant genes. The materials needed to practice this example are: total or messenger RNA, primer, Superscript II buffer, dithiothreitol (DTT), nucleotide mix, Cy3 or Cy5 dye, Superscript II (RT), ammonium acetate, 70% EtOH, PCR machine, and ice.

25 The volume of each sample that would contain 20µg of total RNA (or 2µg of mRNA) is calculated. The amount of DEPC water needed to bring the total volume of each RNA sample to 14 µl is also calculated. If RNA is too dilute, the samples are concentrated

to a volume of less than 14  $\mu$ l in a speedvac without heat. The speedvac must be capable of generating a vacuum of 0 Milli-Torr so that samples can freeze dry under these conditions. Sufficient volume of DEPC water is added to bring the total volume of each RNA sample to 14  $\mu$ l. Each PCR tube is labeled with the name of the sample or control 5 reaction. The appropriate volume of DEPC water and 8  $\mu$ l of anchored oligo dT mix (stored at -20°C) is added to each tube.

Then the appropriate volume of each RNA sample is added to the labeled PCR tube. The samples are mixed by pipeting. The tubes are kept on ice until all samples are ready for the next step. It is preferable for the tubes to kept on ice until the next step is ready to 10 proceed. The samples are incubated in a PCR machine for 10 minutes at 70°C followed by 4°C incubation period until the sample tubes are ready to be retrieved. The sample tubes are left at 4°C for at least 2 minutes.

The Cy dyes are light sensitive, so any solutions or samples containing Cy-dyes should be kept out of light as much as possible (i.e. cover with foil) after this point in the 15 process. Sufficient amounts of Cy3 and Cy5 reverse transcription mix are prepared for one to two more reactions than would actually be run by scaling up the following protocols:

For labeling with Cy3

8 ul 5x First Strand Buffer for Superscript II  
20 4 ul 0.1 M DTT  
2 ul Nucleotide Mix  
2 ul of 1:8 dilution of Cy3 (i.e., 0.125mM Cy3 dCTP).  
2 ul Superscript II

For labeling with Cy5

25 8 ul 5x First Strand Buffer for Superscript II  
4 ul 0.1 M DTT  
2 ul Nucleotide Mix  
2 ul of 1:10 dilution of Cy5 (i.e., 0.1mM Cy5 dCTP).  
2 ul Superscript II

About 18  $\mu$ l of the pink Cy3 mix is added to each treated sample and 18  $\mu$ l of the 30 blue Cy5 mix is added to each control sample. Each sample is mixed by pipeting. The samples are placed in a PCR machine for 2 hours at 45°C followed by 4°C until the sample

tubes are ready to be retrieved. The samples are transferred to Eppendorf tubes containing 600 µl of ethanol precipitation mixture. Some of the EtOH precipitation mixture is used to rinse the PCR tubes. The tubes are inverted to mix. Samples are placed in -80°C freezer for at least 20-30 minutes. If desired, samples may be left at -20°C overnight or over the

5 weekend.

The samples are centrifuged for 15 minutes at 20800 x g (14000 rpm in Eppendorf model 5417C) and carefully the supernatant is decanted. A visible pellet is seen (pink/red for Cy3, blue for Cy5). It is preferable to centrifuge the tubes at a fixed position so the pellet will be at a known area in the tube. In some rare instances, the probe is seen spread 10 on one side of the tube instead of a tight pellet. If the pellet is white or nonexistent, the reaction has not occurred to maximal efficiency.

Ice cold 70% EtOH (about 1 ml per tube) is used to wash the tubes and the tubes are subsequently inverted to clean tube and pellet. The tubes are centrifuged for 10 minutes at 20800 x g (14000 rpm in Eppendorf model 5417C), then the supernatant is carefully 15 decanted. The tubes are flash spun and any remaining EtOH is removed with a pipet. The tubes are air dried for about 5 to 10 minutes. protected from light. The length of drying time will depend on the natural humidity of the environment. For example, an environment in Santa Fe would require about 2 to 5 minutes of drying time. It is preferable that the pellet are not overdried.

20 When the pellets are dried, they are resuspended in 80 ul nanopure water. The cDNA/mRNA hybrid is denatured by heating for 5 minutes at 95°C in a heat block and flash spun.

To purify fluorescence-labeled first strand cDNA probes, the following materials are used: Millipore MAHV N45 96 well plate, v-bottom 96 well plate (Costar), Wizard 25 DNA binding Resin, wide orifice pipette tips for 200 to 300 µl volumes, isopropanol, nanopure water. It is highly preferable to keep the plates aligned at all times during

centrifugation. Misaligned plates lead to sample cross contamination and/or sample loss. It is also important that plate carriers are seated properly in the centrifuge rotor.

The lid of a "Millipore MAHV N45" 96 well plate is labeled with the appropriate sample numbers. A blue gasket and waste plate (v-bottom 96 well) is attached. Wizard DNA Binding Resin (Promega cat#A1151) is shaken immediately prior to use for thorough resuspension. About 160 µl of Wizard DNA Binding Resin is added to each well of the filter plate that is used. If this is done with a multi-channel pipette, wide orifice pipette tips would have been used to prevent clogging. It is highly preferable not to touch or puncture the membrane of the filter plate with a pipette tip. Probes are added to the appropriate wells (80 µl cDNA samples) containing the Binding Resin. The reaction is mixed by pipeting up and down ~10 times. It is preferable to use regular, unfiltered pipette tips for this step. The plates are centrifuged at 2500 rpm for 5 minutes (Beckman GS-6 or equivalent) and then the filtrate is decanted. About 200 µl of 80% isopropanol is added, the plates are spun for 5 minutes at 2500 rpm, and the filtrate is discarded. Then the 80% isopropanol wash and spin step is repeated. The filter plate is placed on a clean collection plate (v-bottom 96 well) and 80 µl of Nanopure water, pH 8.0-8.5 is added. The pH is adjusted with NaOH. The filter plate is secured to the collection plate with tape to ensure that the plate did not slide during the final spin. The plate sat for 5 minutes and is centrifuged for 7 minutes at 2500 rpm. If there are replicates of samples they should be pooled.

To semi-quantitatively assess the incorporation of fluorescence into cDNA probes and to concentrate probes prior to hybridization, the following material is used: 384 well, 100 µl assay plate (Falcon Microtest cat#35-3980) and Wallac Victor 1420 Multilabel counter (or equivalent).

It is preferable that a consistent amount of cDNA is pipeted into the 384-well plate wells because readings will vary with volume. Controls or identical samples should be pooled at this step, if required. The probes are transferred from the Millipore 96 well plate to every other well of a 384 well assay plate (Falcon Microtest). This is done using a multi-

channel pipette. For replicate samples that have been pooled, 60  $\mu$ l aliquots are transferred into wells of the assay plate.

The Cy-3 and Cy-5 fluorescence is analyzed using the Wallac 1420 workstation programmed for reading Cy3-Cy-5 in the 384-well format and the data is saved to disk.

- 5      The typical range for Cy-3 (20 $\mu$ g) is 250-700,000 fluorescence units. The typical range for Cy-5 (20 $\mu$ g) is 100-250,000 fluorescence units. Settings for the Wallac 1420 fluorescence analyzer are as follows:

Cy3

- 10     CW lamp energy        = 30445  
Lamp filter                = P550 slot B3  
Emission filter= D572 dysprosium slot A4  
Emission aperture        = normal  
Count time                = 0.1 s

15     Cy5

- 20     CW lamp energy        = 30445  
Lamp filter                = D642 samarium slot B7  
Emission filter= D670 slot A8  
Emission aperture        = normal  
Count time                = 0.1 s

The dry-down process of the probes is as follows. Concentration of the cDNA probes is highly preferable so that they can be resuspended in hybridization buffer at the appropriate volume. The volume of the control cDNA (Cy-5) is measured and divide by the number of samples to determine the appropriate amount to add to each test cDNA (Cy-

- 25     3). Eppendorf tubes are labeled for each test sample and the appropriate amount of control cDNA is allocated into each tube. The test samples (Cy-3) are added to the appropriate tubes. These tubes are placed in a speed-vac to dry down, with foil covering any windows on the speed vac. At this point, heat (45°C) may be used to expedite the drying process. Time will vary depending on the machinery. The drying process takes about one hour for  
30     150  $\mu$ l samples dried in the Savant. Samples may be saved in dried form at -20°C for up to 14 days.

To hybridize labeled cDNA probes to single stranded, covalently bound DNA target genes on glass slide microarrays, the following material are used: formamide, SSC, SDS, 2  $\mu$ m syringe filter, salmon sperm DNA, hybridization chambers, incubator, coverslips, parafilm, heat blocks. It is preferable that the array is completely covered to ensure proper hybridization.

5 About 30  $\mu$ l of hybridization buffer is prepared per sample. Slightly more than is what is needed should be made since about 100  $\mu$ l can be lost during filtration.

	<u>Hybridization Buffer:</u>	<u>for 100 <math>\mu</math>l:</u>
10	• 50% Formamide	50 $\mu$ l formamide
	• 5X SSC	25 $\mu$ l 20X SSC
	• 0.1% SDS	25 $\mu$ l 0.4% SDS

The solution is filtered through 0.2  $\mu$ m syringe filter, then the volume is measured.

15 About 1  $\mu$ l of salmon sperm DNA (10mg/ml) is added per 100  $\mu$ l of buffer. Materials used for hybridization are: 2 Eppendorf tube racks, hybridization chambers (2 arrays per chamber), slides, coverslips, and parafilm. About 30  $\mu$ l of nanopure water is added to each hybridization chamber. Slides and coverslips are cleaned using N<sub>2</sub> stream. About 30  $\mu$ l of hybridization buffer is added to dried probe and vortexed gently for 5 seconds. The probe remained in the dark for 10-15 minutes at room temperature and then is gently vortexed for several seconds and then is flash spun in the microfuge. The probes are boiled for 5 minutes and centrifuged for 3 min at 20800 x g (14000 rpm, Eppendorf model 5417C).

20 Probes are placed in 70 °C heat block. Each probe remained in this heat block until it is ready for hybridization.

25 Pipette 25  $\mu$ l onto a coverslip. It is highly preferable to avoid the material at the bottom of the tube and to avoid generating air bubbles. This may mean leaving about 1  $\mu$ l remaining in the pipette tip . The slide is gently lowered, face side down, onto the sample so that the coverslip covered that portion of the slide containing the array. Slides are

placed in a hybridization chamber (2 per chamber). The lid of the chamber is wrapped with parafilm and the slides are placed in a 42°C humidity chamber in a 42°C incubator . It is preferable to not let probes or slides sit at room temperature for long periods. The slides are incubated for 18-24 hours.

5 To obtain single stranded cDNA probes on the array, all non-specifically bound cDNA probe should be removed from the array. Removal of all non-specifically bound cDNA probe is accomplished by washing the array and using the following materials: slide holder, glass washing dish, SSC, SDS, and nanopure water. It is highly preferable that great caution be used with the standard wash conditions as deviations can greatly affect  
10 data.

Six glass buffer chambers and glass slide holders are set up with 2X SSC buffer heated to 30-34°C and used to fill up glass dish to 3/4th of volume or enough to submerge the microarrays. It is important to exercise caution in heating of the 2X SSC buffer since a temperature of greater than 35°C might strip off the probes. The slides are removed from  
15 chamber and placed in glass slide holders. It is preferable that the slides are not allowed dry out. The slides are placed in 2X SSC buffer but it is recommended that no more than 4 slides be placed per dish. Coverslips should fall off within 2 to 4 minutes. In the event that the coverslips do not fall off within 2 to 4 minutes, very gentle agitation may be administered. The stainless steel slide carriers are placed in the second dish and filled with  
20 2X SSC, 0.1%SDS. Then the slides are removed from glass slide holders and placed in the stainless steel holders submerged in 2X SSC, 0.1%SDS and soaked for 5 minutes. The slides are transferred in the stainless steel slide carrier into the next glass dish containing 0.1X SSC and 0.1%SDS for 5 minutes. Then the slides are transferred in the stainless steel carrier to the next glass dish containing only 0.1X SSC for 5 minutes. The slides, still in  
25 the slide carrier, is transferred into nanopure water (18 megaohms) for 1 minute.

To dry the slides, the stainless steel slide carriers are placed on micro-carrier plates with a folded paper towel underneath. The top of the slides are gently dabbed with a tissue.

Then the slides are spun in a centrifuge (Beckman GS-6 or equivalent) for 5 minutes at 1000 rpm. It is very important that the slides do not air dry, as this will lead to increased background.

When the examples are practiced by a skilled artisan as disclosed, an analysis of a toxicological response to an agent, for example, cadmium chloride, can be obtained.

#### Preparation of cDNA

The following materials were used to prepare cDNA from RNA: total or messenger RNA; 3DNA™ Submicro™ Expression Array Detection Kit (Genisphere 3DNA 14 Phillips Parkway Montvale, NJ 07645; Kit numbers: K20F00-41 and K20F00-31); Linear Acrylamide (Ambion); RNase free water (Ambion); 0.5M NaOH/50mM EDTA; 1M Tris-HDI, pH 7.5; 10mM Tris pH 8/1mM EDTA; 3M Ammonium Acetate; 70% Ethanol (Aldrich); 100% Ethanol (Aldrich); Denhardt's Salmon Sperm DNA (Sigma); RNase Zap (Ambion); Thermal Cycler; -80°C Freezer; Heat block; 4°C Microfuge; SpeedVac; MicroArray slides; Coverslips; Hybridization Chamber; 42°C Humidity Chamber; Parafilm.

For synthesis of cDNA, prepare 2 separate identical reactions for each sample. In a PCR or 1.5ml tube combine: 1.5ug lymphocyte RNA in 7ul DEPC treated water (if sample is too dilute, concentrate it in the SpeedVac at room temperature), and 3ul RT Primer. Separate tubes for treated and untreated RNA. Heat mixture to 80°C for 10 minutes, 4°C for 2 minutes. Place samples on ice and add the following: 4ul 5X RT buffer, 1ul dNTP mix, 4ul RNase free water, and 1ul Reverse transcriptase enzyme. Gently mix and centrifuge the contents of the tube. Incubate at 42°C for 1.5 to 2 hours. Stop the reaction by adding 3.5ul of 0.5M NaOH/50nM EDTA. Incubate at 65°C for 10 minutes to denature the DNA/RNA hybrids. Neutralize the reaction with 5ul of 1M Tris-HCL, pH 7.5. Transfer to 1.5ml tube if in PCR tube and add 38.5ul of 10mM Tris, pH8/1mM EDTA. Precipitate by adding the following to each tube: 4ul Linear acrylamide, 175ul 3M

Ammonium Acetate, and 625ul 100% Ethanol. Incubate at -80°C for 30 minutes. Centrifuge at 13,000 rpm in 4°C centrifuge for 15 minutes. Carefully decant supernatant.

### 11. Taqman® RT Reaction

5       Taqman® technology from Roche Molecular System was used in the following manner. The mRNA was converted to cDNA using 3µg total RNA and 1.5µl random hexamer primers. After a 10 minute incubation at 70°C the following components were added to the reaction mixture: 6µl of 5x first strand buffer, 3µl 0.1 DTT, 1.5µl 10mM dNTPs, 1.5µl Superscript enzyme and 6.5µl DEPC-treated water. The reaction is  
10      incubated for two hours at 45°C and 1µl of this reaction is used for the Taqman® assay. For the Taqman® assay 50µl reactions were set up with Rnase-free water, Taqman® Universal PCR Master Mix, target and control primers /probes and cDNA.

Real time PCR can be performed using the Taqman® assay . The method measures PCR product accumulation with a dual-labeled fluorogenic probe. The probes  
15      are labeled with 6-FAM on the 5' end and TAMRA on the 3' end. TAMRA is a quencher dye. This assay exploits the 5'-3' exonuclease property of Taq polymerase. When the probe hybridizes to its target the reporter dye (FAM) is cleaved by the 5' exonuclease activity of the Taq polymerase and can emit a fluorescent signal. With increasing cycles of amplification more signal is emitted and detected using an ABI 7700 sequence detector.  
20      For each gene, a set of two primers and a fluorogenic probe are designed and synthesized. For quantitation of mRNA the best design for probes and primers requires primers to be positioned over exon-intron junctions. This rules out amplification of contaminating genomic DNA. For initial studies, primer and probe sets have been designed for 13 genes that were up- or down-regulated by penicillin in differential display experiments. The  
25      probes and primer sets were tested for their ability to amplify genomic DNA. If genomic DNA was amplified, the probes and primers for that particular gene were not used for the Taqman® assay. Figure 9 and 10 show results obtained with a penicillin sensitive person

as well as a penicillin refractive person. The genes in these figures are as follows: 1A is Inhibitor of apoptosis protein-1, 76B is cyclin D2, 142B is Fc-gamma-receptorIIA (FCGR2A), 167B is chromosome 16 clone, RP11-296I10 198A is ribosomal protein S24 (RPS24a), 198B is ribosomal protein S24 (RPS24a). The Y-axis refers to levels of gene expression based on ABI Prism 7700 Realitive Quantification Software, in which cDNA levels are measured based on Ct (Cycle Threshold) values between control and treated samples.

5                   Example8: Differential Protein Expression in Penicillin Treated and Untreated Human Lymphocytes from Penicillin Sensitive and Refractive Individuals

10                  Protein expression in lymphocytes was studied using two technologies, SDS Polyacrylamide Electrophoresis (SDS-PAGE) and Surface Enhanced Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (SELDI-TOF) of proteins applied to ProteinChips. Differences in protein profiles, treated and untreated, for sensitive and refractive samples were observed using both techniques. The following methods were used:

15                  Cell Preparation

20                  For these experiments, blood was drawn from four refractive (control) individuals and two penicillin-sensitive individuals. White blood cells were isolated and cultured for 24 hours, using standard cell culture conditions. The cultures were split, half the cells were treated with penicillin, and all cells were grown for an additional 24 hours. Media was removed by centrifugation. Cells were then subjected to hypotonic lysis in nanopure water, followed by centrifugation to remove solid cellular debris. The supernatants were frozen prior to protein experiments. Cell lysates were concentrated by vacuum centrifugation prior to SDS-PAGE and ProteinChip experiments.

25                  SDS-PAGE

Proteins were electrophoresed using a Bio-Rad MiniProtean gel apparatus, on ReadyGel Precast 4-20% acrylamide gels, using the standard method of Laemmli. For each concentrated lysate, 20 ul sample was mixed with 5 ul 5X SDS sample buffer. The samples were boiled for 10 minutes in the presence of 2-mercaptoethanol and half of each 5 sample was loaded into corresponding wells on two identical gels. Two stains were used to visualize proteins in the replicate gels, Coomassie Blue and Ruby SYPRO (BioRad). Bands were observed directly for Coomassie stained gels, and by fluorescence scanning (Hitachi Scanner) for Ruby stained gels. All gels were dried in cellophane membranes as permanent records stored in (the laboratory notebook).

10

#### ProteinChip/SELDI-TOF

ProteinChips were obtained from Ciphergen Biosystems. Chips containing spots with hydrophobic (H4) and normal phase (NP) chromatographic surfaces were used. For the H4 surface, 1 ul acetonitrile was pipetted onto each spot to pre-wet the C-18 surface. 15 Nanopure water was used to wet the normal phase chip. Three microliters of concentrated lysate was added to each spot on replicate chips, with eight spots/samples per chip. The spots were dried at room temperature, then washed with 10% acetonitrile and nanopure water, for the H4 and NP chips, respectively. Washes were performed by pipetting 5 ul wash solution onto each spot, allowing a 5 minute incubation to resolubilize 20 non-specifically bound biomolecules, and pipetting in and out five times prior to removing the wash buffer. Spots were dried under a 100 Watt bulb (placed 2 feet above benchtop). Each spot was then treated with 0.5 ul sinapinic acid (saturated in 50% acetonitrile, 0.5% trifluoroacetic acid), which acts as an energy absorbing "matrix" to assist laser ionization of proteins. Proteins were detected directly from the chips using a PBS-II mass spectrometer 25 (Ciphergen Biosystems). Spectra were electronically stored in powerpoint files.

#### Results

Using both techniques, differences were observed in the protein profiles of treated and untreated, sensitive and refractive samples. The SDS-PAGE 1-D data is low resolution, but clearly shows increased production of at least four proteins in penicillin-treated sensitive cells, compared with the controls. Sensitivity was comparable for SELDI-  
5 TOF on ProteinChips is a more sensitive technique, and showed hundreds of peaks in each profile. The differences in protein spectra were striking, showing that refractive cells exhibit protein induction that is different than the induction in sensitive cells. While many differences were observed (at least 5-10 proteins), the similarities in the overall profiles  
10 was striking, and permits reasonable difference comparison by providing internal standards.

**TABLE 1**

<b>Generic Name</b>
acetaminophen
acetaminophen/codeine
acetohydroxamic acid
actinomycin D
acyclovir
adenosine
albuterol
alendronate
alendronate sodium
alglucerase
allopurinol
alosetron
alprazolam
alprostadiol
alteplase
ambenonium
amifostine
amiloride
aminobenzoate potassium
aminoglutethimide
aminopurine
aminosalicylate sodium
amiodorone
amitriptyline
amlodipine
amoxapine
amoxicillin
amphetamine mixed salts
ampicillin
amprenavir
amyl nitrite
anagrelide
ancrod
androgens
anistreplase
anthralin
araC
aspirin
aspirin
astemizole
atenolol
atorvastatin

atovaquone
atropine
attapulgite
azathioprine
azelastine
azithromycin
aztreonam
bacampicillin
baclofen
beclomethasone
belladonna
benazepril
benazepril
benzodiazepines
benzoyl peroxide
benztropine
beta carotene
betamethasone
betamethasone
betamethasone valerate
bethanechol
bisacodyl
bismuth subsalicylate plus
bisoprolol/HCTZ
bleomycin
bradykinin antagonist
bromfenac
brominide tartrate
bromocriptine
bronchodilators
bucizine
budesonide
bumetanide
bupropion HCL
buspirone
busulfan
calcipotriene
calcitonin salmon
calfactant
candesartan cilexetil
capsaicin
captopril
carbamazapine
carbenicillin
carbidopa
carboplatin

carisoprodol
carmustine
carvedilol
cefaclor
cefepime
cefprozil
ceftibuten
cefuroxime
celecoxib
cephalexin
cephalosporins
cerivastatin
cetirizine
chenodiol
chlophedianol
chloral hydrate
chlorambucil
chloramphenicol
chloroquine
chlorpropamide
chlorthalidone
chlorzoxazone
cholestyramine
cimetidine
cinoxacin
ciprofloxacin
(+)-cis-3,5-dimethyl-2-(3-pyridyl)thiazolidin-4
cisapride
cisplatin
citalopram
clarithromycin
clavulanate
clavulanate
clavulanic acid
clidinium
clindamycin
clofibrate
clomiphene
clonazepam
clonidine
clotrimoxazole
cloxacillin
clozapine
codeine
colchicine

colestipol
collagen-alginate
conjugated estrogens
copolymer-1
cortisone
courmarin
cromolyn
cyclacillin
cyclandelate
cyclizine
cyclobenzaprine
cyclopegic
cyclopentolate
cyclophosphamide
cycloserine
cyclosporine
cyclosporine A
cytoxin
dalteparin injection
danazol
dantrolene
dapsone
daunomycin
daunorubicin
dehydrocholic acid
desmopressin
desogestrel
dexamethasone
dextromethorphan
dextrothyroxine
diazepam
diazoxon
dichloralphenazone
diclofenac
diclofenac dihydrazine
dicloxacillin
dicyclomine
didanosine
difenoxin
digitalis glycosides
digoxin
dihydrazine
dihydroergotamine mesylate
dihydrolazine
diltiazem
dimethyl sulfoxide

dinoprostone
dione
diphenidol
diphenoxylate
dipyridamole
dipyridamole
disopyramide
disulfiram
divalproex
divalproex sodium
docusate sodium
dolasetron mesylate
donepezil
doxazosin
doxercalciferol
doxorubicin
doxycycline
enalapril
enoxaparin
entacapone
ephedrine
epirubicin
eptifibatide
ergoloid mesylates
ergonovine
erythromycin
estradiol
estramustine
etanercept
ethacrynic acid
ethchlorvynol
ethinamate
ethinyl estradiol
ethinyl estradiol
ethionamide
etidronate
etoposide
etretinate
exemestane
famciclovir
famotidine
felbamate
felodipine
felodipine SR
fenofibrate
fenoldopam mesylate

fentanyl citrate
fexofenadine
fialuridine
finasteride
flavoxate
flecainide acetate
flosequinan
fluconazole
flunisolide
fluoroquinolones
fluorouracil .
fluoxetine
flutamide
fluticasone
fluticasone
fluticasone propionate
fluvastatin
fluvoxamine maleate
foscarnet sodium
fosinopril
fosphenytoin
furazolidone
furosemide
gabapentin
ganciclovir
ganirelix acetate
gemcitabine
gemfibrozil
glimepiride
glipizide
glucagon
glyburide
glycopyrrolate
gold compounds
gold sodium thiomalate
granisetron
grepafloxacin
griseofulvin
guaifenesin
guanabenz
guanadrel
guanethidine
guanfacine
haloperidol
heparin
hismanol

hydantoin
hydralazine
hydrochlorothiazide
hydrocodone
hydrocortisone
hydroxychloroquine
hydroxyurea
hydroxyzine
hyoscine
hyoscyamine
hyoscyamine
hyperozia
ibuprofen
ibutilide fumarate
imiglucerase injection
imiquimod 5% cream
inactivated hepatitis A vaccine
indapamide
indinavir
indomethacin
insulin
interferon-beta-1a (recombinant)
interferon-beta-1b (recombinant)
iodinated glycerol
iodoquinol
ipecac
iphosphamide
ipratropium
irbesartan
irinotecan
isomethoptene
isoniazid
isoproterenol
isosorbide mononitrate S.A.
isotretinoin
isoxsuprine
isradipine
itraconazole
kanamycin
ketoconazole
ketorolac
lactulose
lamivudine, 3TC
lamotrigine
lansoprazole
latamoxef

latanoprost
leflunomide
letrozole
leucovorin
leuprolide
levamisole
levetiracetam
levobupivacaine
levocabastine
levocarnitine
levodopa
levofloxacin
levonorgestrel
levothyroxine
lidocaine
lincomycin
liposomal amphotericin B
lisinopril
lispro insulin
lithium
I-norgestrel
I-norgestrel/ethynodiol estradiol
lomustine
loperamide
loracarbef
loratadine
Loratadine/Pseudoephedrine
lorazepam
losartan
lovastatin
loxapine
magnesium sulfate
maprotiline
masoprocol
mazindol
mecamylamine
mechlorethamine
meclizine
medroxyprogesterone
medroxyprogesterone
mefloquine
melatonin
melphalan
menotropin
meprobamate
merbarone

mercaptopurine
meropenem
mesalamine
metformin
methenamine
methicillin
methotrexate
methylcellulose
methyldopa
methylergonovine
methylphenidate
methylprednisolone
methyprylon
methysergide
metoclopramide
metoprolol
metoprolol
metronidazole
metyrapone
metyrosine
mexiletine
mibepradil
miconazole cream 2%
miglitol
minocycline
minoxidil
misoprostol
misoprostol
mitotane
mixed amphetamines
moclobemide
molindone
mometasone
moricizine
moxifloxacin
mupirocin
nabilone
nabumetone
nafarelin
nafcillin
nalidixic acid
naltrexone
naproxen
naratriptan
natamycin
navirapine

nedocromil
nefazodone
neomycin
Neomycin/Polymx/HC
neostigmine
nicardipine
nicorandil
nicotine
nifedipine
nimodipine
nitrofurantoin
nitroglycerin
nizatidine
norethindrone
norethindrone/ ethinyl estradiol
norgestimate
norgestimate/ethinyl estradiol
norgestrel
norgestrel/ethinyl estradiol
nylidrin
nystatin
ofloxacin
olsalazine
omeprazole
orphenadrine
oxacillin
oxaprozin
oxatriphylline
oxybutynin
oxycodone
oxymetazoline
paclitaxel
pancreatin
pancrelipase
papaverine
paraldehyde
paramethasone
paregoric
paroxetine
pediculicides
pemoline
penicillamine
penicillin
pentamidine
pentoxifylline
pepsin

pergolide
perhexiline
perindopril
perphenazine
pexiganan acetate
phenazopyridine
phendimetrazine
phenformin
phenobarbital
phenolphthalein
phenothiazines
phentermine
phenylephrine
phenylephrine
phenylpropanolamine
phenylpropanolamine
phenytoin
pilocarpine
pioglitazone
piroxicam
podophyllum
poloxamer 188
polycarbophil calcium
Polyethylene glycol
polythiazide
potassium chloride
potassium iodide
potassium phosphates
pramipexole
pravastatin
prazosin
prednisolone
prednisone
primaquine
primethamine
primidone
probencid
probucol
procainamide
procarbazine
progesterins
promethazine
propafenone
propantheline
propoxyphene
propranolol

propulsid
pseudoephedrine
psoralens
psyllium
pyridostigmine
pyridoxine (vitamin b-6)
quinacrine
quinapril
quinidine
quinine
rabeprazole
raloxifene
ramipril
ranitidine
recombinant clotting factor VIII
recombinant interferon alpha-2b
recombinant OspA
remoxipide
reserpine
rezulin
ribavirin
rifampin
rimantadine
risedronate
risperidone
ritodrine
rosiglitazone
salicylates
salmeterol
saquinavir
scopolamine
seldane
selegiline
sertraline
sibutramine
sildenafil citrate
simethicone
simvastatin
s-mephenytoin
sodium ferric gluconate
soman
somatostatin
sotalol
spironolactone
stanol esters
streptozotocin

succinimide
sucralfate
sulfacytine
sulfadoxine
sulfamethoxazole
sulfamethoxazole
sulfasalazine
sulfinpyrazone
sulfisoxazole
sumatriptan
(s)-warfarin
tacrine
tamoxifen
tamsulosin
telmisartan
temazepam
terazosin
terbinafine HCl
terbutaline sulfate
terfenadine
terpin hydrate
testolactone
tetracycline HCl
tetracyclines
theophylline
thiamine
thiazide
thioguanine
thiopurine
thiothixene
tiagabine
ticlopidine
tienilic acid
timolol
tiopronin
tirofiban
tobramycin
tobramycin/dexamethasone
tocainide
tolbumamide
tolcapone
tolterodine
topotecan
toremifene
tramadol
trandolapril

trastuzumab
trazodone
tretinoin
triamcinolone
triamterene/HCTZ
triamterine
triamterine
triazolam
trihexyphenidyl
trilostane
trimeth/sulfameth
trimethobenzamide
trimethoprim
troglitazone
trovafloxacin
urokinase
ursodiol
valproic acid
valsartan
vancomycin
venlafaxine
verapamil
vincristine
warfarin
xanthine
xylometazoline
zaflukast
zalcitabine
zidovudine
zolpidem

TABLE 2

Industrial Chemicals
1,2-Dibromomethane
2,4-dinitrotoluene
2-methylpentane
3-methylpentane
4,4'-methylene bis
7, 12-dimethylbenz[a]anthracene
Acetone
Acrylamide
Acrylonitrile
Apha methylstyrene
Aluminum
Aniline
Antimony
Arsenic
Barium
Baygon
Benzene
Benzidine
Beryllium
Bta-naphthylamine
Biphenyl
Cadmium
Carbamate(s)
Carbaryl
Carbon disulfide
Carbon monoxide
Carbon tetrachloride
Chloroform
Chromium VI
Cobalt
Copper
Cumene
Cyanamide
Cyanides
Cyclohexane
Cyclohexanone
Cyclophosphamide
DDT
DEHP
Dichlorobenzene
Dichloromethane

Dieldrin
Diethylamine
Diethylstilbestrol
Dimethylacetamide
Dimethylformamide
Dinitroorthocresol
Dioxane
Endrin
Enflurane
Ethylbenzene
Ethylene oxide
Ethyleneglycol dinitrate
Ethyleneglycol(s)
Fluoride
Furfural
Furfuryl alcohol
Germanium
Halothane
Hexachlorobenzene
Hexachlorobutadiene
Isopropanol
Isopropylnitrate
Lead
Lead tetraethyl
Lindane
Maleic anhydride
Manganese
Mercury
Methanol
Methylchloride
Methylethylketone
Methylmercury
Monobromomethane
Monochlorobenzene
n-hexane
Nickel
Nitrobenzene
Nitroglycerine
Nitrous oxide
Organophosphorus
Parathione
Pentachlorophenol
Phenol
Phtalic anhydride
Polychlorinated biphenyl
Polycyclic hydrocarbons

Propyleneglycol
Selenium
Silver
Stryrene
Synthetic pyrethroids
T-butylhydroperoxide
TCDD
Tellerium
Tert-butylphenol
Tetrachloroethylene
Thalium
Toluene
Toluene diisocyanate
Trichloroethane
Trichloroethylene
Triethylamine
Triethylbenzenes
Uranium
Vanadium
Vinyl chloride
Xylene
Zinc

TABLE 3

Gene Name	Genbank Accession No.
Ataxia telangiectasia	U33841
ATF4 (activating trxn factor 4)	D90209
ATP-dep. Helicase II (70kDa)	M32865
ATP-dep. Helicase II (Ku80)	M30938
Bax (alpha)	L22473
Bcl-xL	Z23115
c-Abl	M14752
c-Fos	K00650
Chk1	AF016582
c-H-Ras	J00277
c-Jun	J04111
Clusterin (serum protein 40)	X14723
c-Myc	X00364
Connexin 32 (gap junction protein)	X04325
Cyclin G	D78341
Cytochrome P-1-450 (cyp1A1)	K03191
DNA binding protein inhibitor ID-2	D13891
DNA dependent helicase	L36140
DNA dependent protein kinase	U47077
DNA ligase IV	X83441
DNA polymerase alpha	X06745
DNA repair protein (Rad 50)	U63139
DNA repair protein XRCC1	M36089
DNA topoisomerase I	J03250
ERCC1 (excision repair protein)	M13194
DNA repair helicase II ERCC-3	M31899
Excision repair ERCC-5	L20046
Gadd153	S40706
Gadd45	M60974
Glutathione Peroxidase	M21304
HDLC1	U32944
Hsp70	M11717
Hsp90	X15183
ICE Rel II	U28014
Mdm-2	U33199
Mdr-1	M14758
MnSOD	Y00985
Mut S homologue (hMSH2)	U04045
MUTL homolog=hMLH1	U07418
Poly (ADP-ribose) polymerase (PARP)	M32721/X56140
Prolifer.cell nuclear antigen (PCNA)	J04718
RAD	L24564

RAD51 homolog	D13804
RNA-dependent Helicase (DEAD-box protein p72)	U59321
SQM1	M33374
Stress activated protein kinase JNK1	L26318
UV Excision repair protein RAD23 (XP-C)	D21090
Vascular cell adhesion molecule 1 (VCAM-1)	M73255
Alpha-Tubulin	K00558
Beta-Actin	X00351
Glucose-6-phosphate dehydrogenase (G6PD)	X03674
cytochrome p-450 4A	L04751
connexin 40	L34954
Bak	U16811
Collagenase, type I interstitial	X54925
G/T mismatch binding protein	U28946
Mismatch repair/binding protein (hMSH3)	U61981
DNA mismatch repair protein (hPMS2)	U14658
Apolipoprotein A-II	M29882
Acyl CoA dehydrogenase	U12778
Carnitine palmitoyl CoA transferase	M58581
Hepatic lipase	J03540
Ornithine decarboxylase	M16650
Superoxide dismutase Cu/Zn (SOD)	K00065
Ref-1:redox factor	S43127
Thioredoxin	J04026
Glutathione synthetase	L42531
Glutathione reductase	X15722
Thymidine kinase	K02581
Bag-1=bcl-2	S83171
BRCA1	U14680
Phenol sulfotransferase	U26309
Aldehyde dehydrogenase 1 (ALDH-1)	K03000
Aldehyde dehydrogenase 2 (ALDH-2)	K03001
12-lipoxygenase	M58704
Phospholipase A2	M86400
Calnexin	M94859
Apolipoprotein CIII.	X01388
Branched chain Acyl-CoA Oxidase	X95190
Cyclin dependent kinase 4 (cdk4)	M14505
ERp72	J05016
MCL-1	L08246
HMG CoA reductase	M11058
Lipopolysaccharide binding protein	M35533
Lysyl oxidase	M94054
Farnesol Receptor	U68233
Osteopontin	J04765
P38 mitogen activated protein (MAP) kinase	L35253
Peroxisomal acyl-CoA oxidase	X71440

Uncoupling protein 2 (UCP2)	U82819
Very-long-chain acyl-CoA dehydrogenase	D43682
Vimentin	X56134
EGR1	X52541
GRP94	X15187
P53	K03199
Defender against cell death-1	D15057
Hypoxanthine-guanine phosphoribosyltransferase	V00530
Aspartate aminotransferase, mitochondrial	M22632
Creatine kinase B	L47647
Peroxisome assembly factor-1	M86852
T-cell cyclophilin	Y00052
Transferrin	M12530
UDP-glucuronosyltransferase 2B	AF016492
Octamer-binding protein 1	X13403
E-cadherin	L08599
Catalase	X04076
11 beta-hydroxysteroid dehydrogenase type II	U14631
Bilirubin UDP-glucuronosyltransferase isozyme 1	M57899
Calreticulin	M84739
Calcineurin-B	M30773
Catechol-O-methyltransferase	M58525
Fas antigen	M67454
DNA repair and recombination homologue (RAD52)	L33262
Flavin-containing monooxygenase 1	M64082
Gamma-glutamyl transpeptidase	L20490
Insulin-like growth factor binding protein 1	M31145
Oxygen-regulated protein 150	U65785
Thymidylate synthase	X02308
Biliverdin reductase	U34877
Adenine nucleotide translocator 1	J02966
Hepatocyte nuclear factor 4	X76930
RANTES	M21121
Phosphoglycerate kinase	V00572
PAPS synthetase	Y10387
Plasminogen activator inhibitor 2	M18082
Enolase alpha	M14328
Interferon inducible protein 15	M13755
Insulin-like growth factor I	M37484
Platelet/endothelial cell adhesion molecule-1	M28526
60S ribosomal protein L6	X69391
FosB	L49169
Alpha-catenin	D13866
FEN-1 (endonuclease)	L37374
GOS24 (zinc finger transcriptional regulator)	M92843
Caspase 8 (FLICE)	U58143
Caspase 3 (CPP32-beta)	U13738

Caspase 7 (Mch3-alpha)	U37448
Intercellular adhesion molecule-3	X69819
Phosphoenolpyruvate carboxykinase	X92720
Alpha-1 acid glycoprotein	M13692
IkB-a	M69043
Protein-tyrosine phosphatase	M83738
Ubiquitin conjugating enzyme (Rad6 homolog)	M74524
Alpha-2-macroglobulin	M11313
Zinc finger protein 37	AF022158
Cyclin-dependent kinase inhibitor p27kip1	U10906
Caspase 1	U13697
Organic anion transporter 1	AF057039
Alcohol dehydrogenase 2	M24317
Alchohol dehydrogenase 4	M15943
Annexin V	M21731
Calbindin-D (28kDa)	X06661
Colony-stimulating factor-1	M37435
Hypoxia-inducible factor 1 alpha	U22431
Growth arrest-specific protein 1	L13698
Inhibitor of apoptosis protein-1	AF070674
Nucleic acid binding protein	U19765
OX40 ligand	X79929
Retinoic acid receptor gamma 1	M38258
Cytochrome c oxidase subunit IV	M34600
Glutathione S-transferase theta-1	X79389
Survivin	NM001168
STAT 3	AJ012463
Growth arrest-specific protein 3	L03203
Cyclin D3	M92287
ID-1	X77956
Interleukin-1 beta	X02532
Interleukin-8	Y00787
Monocyte chemotactic protein-1	S69738
Phenylalanine hydroxylase	K03020
Prohibitin	S85655
Cathepsin L	M20496
Transthyretin	X59498
Stromelysin-1	X05232
Spermidine/spermine N1-acetyltransferase (SSAT)	M55580
Ferritin H-chain	L20941
Transferrin receptor	M11507
Ceruloplasmin	M13699
Glucosylceramide synthase	D50840
Leukemia inhibitory factor (LIF)	X13967
Integrin beta-1	X07979
Vascular endothelial growth factor receptor 1 (flt-1)	X51602
Urokinase plasminogen activator receptor (uPAR)	U08839

c-fms	X03663
c-erb B-2	X03363
C5a anaphylatoxin receptor	M62505
FYN proto-oncogene	NM002037
Peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase	L07077
Nucleoside diphosphate kinase beta isoform	X73066
Myelin basic protein	M13577
Peroxisomal 3-oxoacyl-CoA thiolase (=rat peroxisomal 3-ketoacyl-CoA thiolase 2)	X12966
Prostaglandin H synthase	S36271
Retinoid X receptor alpha	NM002957
Interleukin-13	X69079
Tryptophanyl-tRNA synthetase (WRS)	M61715
Silencer of death domains	AF111116
Mannose receptor	J05550
Death receptor 5 (DR5)	AF016268

**Neomycin** **U55761**

**TABLE 4**

(clone hKvBeta3) K<sup>+</sup> channel beta subunit  
APO-1 cell surface antigen  
11-beta hydroxysteroid dehydrogenase type II  
12-lipoxygenase  
17-beta hydroxysteroid dehydrogenase  
25-hydroxyvitamin D3-1 alpha-hydroxylase  
60S ribosomal protein L6  
6-C-kine  
6-O-methylguanine-DNA methyltransferase  
acetylhydrolase IB beta-subunit  
Acid ceramidase  
actin-binding protein (filamin) (ABP-280)  
Activating transcription factor 2  
Activating transcription factor 3  
Activating transcription factor 4  
Activin beta E  
Activin receptor type II  
Acyl - CoA dehydrogenase  
Acyl CoA Carrier Protein  
Adenine nucleotide translocator 1  
Adenylyl cyclase-associated protein (CAP)  
Adhesion protein (SQM1)  
Alanine aminotransferase  
Alcohol dehydrogenase 1  
Alcohol dehydrogenase 2  
Alcohol dehydrogenase 3  
Alcohol dehydrogenase 4  
Alcohol dehydrogenase 7  
Aldehyde dehydrogenase 1  
Aldehyde dehydrogenase 2  
Aldehyde dehydrogenase 3  
Aldose reductase  
Alpha 1-antitrypsin  
Alpha 1-inhibitor III  
Alpha interferon  
Alpha(I)procollagen  
Alpha-1 acid glycoprotein  
Alpha-1 antichymotrypsin  
Alpha-2 macroglobulin  
Alpha-2 microglobulin  
Alpha-catenin  
Alpha-tubulin  
Amyloid protein homologue  
Androgen receptor  
Annexin V

Antiquitin, 26g turgor protein homolog  
Aorta caldesmon  
APC gene  
Apolipoprotein A1  
Apolipoprotein AII  
Apolipoprotein CIII  
Apolipoprotein E  
Aryl hydrocarbon receptor  
Aspartate aminotransferase, mitochondrial  
Ataxia telangiectasia  
ATP Synthase 6  
ATP-dependent helicase II (70kDa)  
ATP-dependent helicase II (Ku80)  
Atrial natriuretic factor  
BAG-1  
BAK  
Bax (alpha)  
Bcl-2  
Bcl-3  
Bcl-xL  
Beta-actin  
Beta-chemokine I-309  
Bile salt export pump (sister of p-glycoprotein)  
Biliary glycoprotein  
Bilirubin UDP-glucuronosyltransferase isozyme 1  
Biliverdin reductase  
B-myb  
Bone morphogenetic protein-4  
Bone sialoprotein gene  
Brain-derived neurotrophic factor  
Branched chain acyl-CoA oxidase  
BRCA1  
BR-cadherin  
Breast basic conserved gene (ribosomal protein L13)  
Breast cancer resistance protein (BCRP)  
C10 beta-chemokine  
C4b-binding protein  
C5a anaphylatoxin receptor  
c-abl  
Calbindin-D (28kDa)  
Calbindin-D (9K)  
Calcineurin-B  
Calnexin  
Calprotectin  
Calreticulin  
canalicular multispecific organic anion transporter

Carbonic Anhydrase III  
Carcinoembryonic antigen (CD66e)  
Carcinoembryonic antigen family member 2  
cardiac gap junction protein  
Carnitine palmitoyl-CoA transferase  
Casein kinase 1 delta  
Caspase 1  
Caspase 2 (Nedd2)  
Caspase 3 (CPP32-beta)  
Caspase 5 (ICE rel-III)  
Caspase 6 (Mch2-alpha)  
Caspase 7 (Mch3-alpha)  
Caspase 8 (FLICE)  
Catalase  
Catechol-O-methyltransferase  
Cathepsin G  
Cathepsin L  
Caveolin-1  
CCAAT/enhancer-binding protein alpha  
CCAAT/enhancer-binding protein epsilon  
CCR-5  
CD44 (metastasis suppressor gene)  
CD64 (Fc gamma)  
Cell division cycle protein 2  
Cell division cycle protein 25  
Cellular retinoic acid binding protein 1  
Cellular retinoic acid binding protein 2  
c-erb B-2  
c-erbA-1  
Ceruloplasmin (ferroxidase)  
c-fms (CSF-1 receptor)  
c-fos  
CHD2  
Checkpoint kinase-1  
Cholesterol esterase  
c-H-ras  
CIG49 (cig49)  
c-jun  
Clone 22 mRNA, alternative splice variant alpha-1  
CLP  
Clusterin  
c-myb  
c-myc binding protein  
Collagen type II  
Colony-stimulating factor-1  
Complement component C3

Connexin 30  
Connexin-32 (aka gap junction protein)  
Connexin-40  
Corticosteroid binding globulin  
Corticotropin releasing hormone  
C-reactive protein  
Creatine kinase B  
Csa-19  
CTCF  
CXCR4  
Cyclin A1  
Cyclin D1  
Cyclin D3  
Cyclin dependent kinase 1  
Cyclin dependent kinase 2  
Cyclin dependent kinase 4  
Cyclin dependent kinase inhibitor 1A  
Cyclin E  
Cyclin G  
Cyclin-dependent kinase 4 inhibitor B (P16)  
Cyclin-dependent kinase inhibitor P27Kip1  
Cyclooxygenase 2  
Cysteine protease CPP32 isoform alpha  
Cystic fibrosis transmembrane conductance regulator  
Cytochrome c oxidase subunit III  
Cytochrome c oxidase subunit IV  
Cytochrome P450 11A1  
Cytochrome P450 17A  
Cytochrome P450 1A1  
Cytochrome P450 1A2  
Cytochrome P450 1B1  
Cytochrome P450 2A1  
Cytochrome P450 2A3  
Cytochrome P450 2A6  
Cytochrome P450 2B1  
Cytochrome P450 2B10  
Cytochrome P450 2B2  
Cytochrome P450 2C11  
Cytochrome P450 2C12  
Cytochrome P450 2C19  
Cytochrome P450 2C9  
Cytochrome P450 2D6  
Cytochrome P450 2E1  
Cytochrome P450 2F2  
Cytochrome P450 3A1  
Cytochrome P450 3A4

Cytochrome P450 4A  
Cytochrome P450 4A1  
cytoskeletal gamma-actin  
Damage-specific DNA binding protein p48  
subunit  
Death receptor 5 (DR5)  
Defender against cell death-1  
Deleted in colorectal cancer  
Delta-like protein  
Diacylglycerol kinase zeta  
Dihydrofolate reductase  
Disulfide isomerase related protein (ERp72)  
DNA binding protein inhibitor ID2  
DNA dependent helicase  
DNA dependent protein kinase  
DNA ligase I  
DNA ligase III  
DNA ligase IV  
DNA mismatch repair protein (MLH1)  
DNA mismatch repair protein (PMS2)  
DNA mismatch repair/binding protein (MSH3)  
DNA polymerase alpha  
DNA polymerase beta  
DNA repair and recombination homologue (RAD 52)  
DNA repair helicase II ERCC-3  
DNA repair protein (RAD 50)  
DNA repair protein (XRCC1)  
DNA replication factor C (36kDa)  
DNA topoisomerase I  
DNA topoisomerase II  
DNA-binding protein (APRF)  
DOC-2  
Dopamine beta-hydroxylase  
Dopamine receptor D2  
DRA  
Dynamin (DNM)  
Dynein light chain 1  
E2F-1  
Early growth regulated protein 1  
E-Cadherin  
ECE-1 (endothelin converting enzyme)  
ELAV-like neuronal protein-2 Hel-N2  
Elongation factor 1-alpha 1 (PTI-1)  
Endothelin-1  
Enolase alpha  
enteric smooth muscle gamma-actin

Eosinophil-derived neurotoxin  
Eotaxin  
Epidermal growth factor  
Epoxide hydrolase  
ERA-B  
ERCC 1 (excision repair protein)  
ERCC 3 (DNA repair helicase II)  
ERCC 5 (excision repair protein)  
ERCC 6 (excision repair protein)  
Erythrocyte membrane protein  
Erythropoietin  
Erythropoietin receptor  
E-Selectin  
Estrogen receptor  
Extracellular-signal-regulated kinase 1  
Farnesol receptor  
Fas antigen  
Fas associated death domain (FADD)  
Fas ligand  
Fas/Apo1 receptor  
Fatty acid synthase  
Fatty acyl-CoA oxidase  
Fatty acyl-CoA synthase  
FEN-1 (endonuclease)  
Ferritin H-chain  
FGF-1  
FGF-7  
Fibrinogen gamma chain  
Fibronectin receptor  
FIC1  
Filaggrin  
Flavin containing monooxygenase 1  
Flavin containing monooxygenase 3  
for gamma-interferon inducible early response  
gene (with homology to platelet proteins)  
FosB  
Fra-1  
Fucosyl transferase (alpha-1,2-  
fucosyltransferase)  
Fyn proto-oncogene  
Gadd153  
Gadd45  
Galanin  
Gamma glutamylcysteinyl synthetase  
Gamma-glutamyl hydrolase (hGH)  
Gamma-glutamyl hydrolase precursor  
Gamma-glutamyl transpeptidase

Garg-16  
GAS-7  
GCLR  
GCLS  
Gelsolin  
Glucocorticoid receptor  
Glucose-6-phosphate dehydrogenase  
Glucose-regulated protein 170  
Glucose-regulated protein 58  
Glucose-regulated protein 78  
Glucose-regulated protein 94  
Glucosylceramide synthase  
Glutamic-oxaloacetic transaminase  
Glutamic-pyruvic transaminase  
Glutamine synthetase  
Glutaredoxin  
Glutathione peroxidase  
Glutathione reductase  
Glutathione S-transferase alpha subunit  
Glutathione S-transferase theta-1  
Glutathione S-transferase Ya  
Glutathione synthetase  
Glyceraldehyde 3-phosphate dehydrogenase  
Gonadotropin (alpha subunit)  
GOS24 (zinc finger transcriptional regulator)  
Granulin  
Granulocyte-macrophage colony-stimulating factor  
Growth arrest-specific protein 1  
Growth arrest-specific protein 3  
GT mismatch binding protein  
Hamartin (TSC1)  
H-cadherin  
Heat shock protein 12  
Heat shock protein 27  
Heat shock protein 47  
Heat shock protein 70  
Heat shock protein 90  
Helicase-like transcription factor  
Heme binding protein 23  
Heme oxygenase-1  
Hemopexin  
Hepatic lipase  
Hepatocyte growth factor  
Hepatocyte growth factor activator  
Hepatocyte nuclear factor 4  
Histamine N-methyltransferase

Histidine decarboxylase  
Histone 2A  
Histone 2B  
Histone deacetylase 1 (HDAC-1)  
hMEF2C, myocyte enhancer-binding factor 2  
HMG CoA reductase  
HMG-I protein isoform mRNA (HMGI gene),  
clone 7C  
Hydroxysteroid sulfotransferase a  
Hypoxanthine-guanine  
phosphoribosyltransferase  
Hypoxia-inducible factor 1 alpha  
ICE-rel II (Caspase 4)  
ID-1  
IkB-a  
immunoglobulin lambda heavy chain  
Immunophilin homolog ARA9  
Inhibitor of apoptosis protein 1  
Inhibitor of apoptosis protein 2  
Insulin-like growth factor binding protein 1  
Insulin-like growth factor binding protein 2  
Insulin-like growth factor binding protein 5  
Insulin-like growth factor binding protein 3  
Insulin-like growth factor I  
Insulin-like growth factor II  
Integrin alpha  
Integrin alpha L  
Integrin beta1  
Integrin beta2  
Integrin beta-4  
Intercellular adhesion molecule-1  
Intercellular adhesion molecule-2  
Intercellular adhesion molecule-3  
Interferon gamma  
Interferon inducible protein 10  
Interferon inducible protein 15  
Interferon stimulatory gene factor-3  
Interleukin-1 alpha  
Interleukin-1 beta  
Interleukin-10  
Interleukin-12  
Interleukin-13  
Interleukin-18  
Interleukin-2  
Interleukin-3  
Interleukin-4  
Interleukin-5

Interleukin-6  
Interleukin-8  
Involucrin  
IRF-7  
Iron permease (FTR1)  
ISG-15  
Jagged 1  
Jagged 2  
JNK1 stress activated protein kinase  
JunB  
JunD  
K+ channel beta 2 subunit  
KAI1 metastasis suppressor gene (CD82)  
K-cadherin  
Keratin 4  
Keratin 6 isoform K6e (KRT6E)  
Keratin K17  
Keratinocyte growth factor  
Ki67  
Ku autoimmune antigen gene (p80)  
L09604  
Lactate Dehydrogenase-B  
Lactoferrin  
Leukemia inhibitory factor (LIF)  
Lipopolysaccharide binding protein  
Lipoprotein lipase precursor  
Liposin  
Liver fatty acid binding protein  
L-myc  
long-chain acyl-CoA synthetase  
Low density lipoprotein receptor  
Lung cancer antigen NY-LU-12 variant A  
Luteinizing hormone  
Lymphoid enhancer-binding factor-1 (LEF-1)  
Lysyl hydroxylase  
Lysyl oxidase  
macropain subunit zeta  
Macrophage inflammatory protein-1 alpha  
Macrophage inflammatory protein-1 beta  
Macrophage inflammatory protein-2 alpha  
Macrophage inflammatory protein-3 alpha  
Macrophage-stimulating protein (MST1)  
Macrostatin  
MAD-related protein 2  
Major acute phase protein alpha-1  
Major basic protein  
Malic enzyme

Mannose receptor  
MAP kinase kinase  
Matrix metalloproteinase-1  
Matrix metalloproteinase-2  
MDM-2  
MET proto-oncogene  
Metallothionein 1  
Metallothionein 2  
Metal-regulatory transcription factor-1  
Metastasis-associated mta1  
Methionine adenosyltransferase (MAT2A)  
MHC class I  
MHC class II  
MHC class II transactivator  
Mim  
Mitochondrial ATP Synthase Subunit E  
mitochondrial short-chain enoyl-CoA hydratase  
Mitochondrial transcription factor 1  
Mitogen activated protein kinase (P38)  
Mitogen inducible gene (mig-2)  
MOAT-B (MRP/organic anion transporter)  
Monoamine oxidase A  
Monoamine oxidase B  
Monocyte chemotactic protein-1  
Monocyte chemotactic protein-1 receptor (CCR2)  
Mr 110,000 antigen  
MSH3 gene  
mss4, Zn<sup>2+</sup> binding protein/guanine nucleotide exchange factor  
Multidrug resistance-associated protein  
Multidrug resistant protein-1  
Multidrug resistant protein-2  
Multidrug resistant protein-3 = cMOAT2  
MUTL homologue (MLH1)  
MutS Homologue (MSH2)  
Myelin basic protein  
Myeloid cell differentiation protein-1  
Myeloid cell leukemia-1 (MCL-1)  
Myeloperoxidase  
Na/taurocholate cotransporting polypeptide  
NADPH cytochrome P450 reductase  
NADPH quinone oxidoreductase-1 (DT-Diaphorase)  
Natural killer cell-enhancing factor B  
N-cadherin  
Neural cell adhesion molecule (N-CAM)  
Neurofibromin (NF1 tumor suppressor)

neuropathy target esterase  
NF-E2  
NF-kappaB (p65)  
Nidogen  
Nitric oxide synthase-1, inducible  
NMB  
Non-specific cross-reacting antigen  
Notch 1  
Nucleic acid binding protein  
Nucleoside diphosphate kinase beta isoform  
nucleosome assembly protein  
O-6-alkylguanine-DNA-alkyltransferase  
OB-cadherin 1  
Octamer binding protein 1  
Octamer binding protein 2  
Oncostatin M  
Organic anion transporter 1  
Organic anion transporter 3  
Organic anion transporter K1  
Organic anion transporting polypeptide 1  
Organic cation transporter 1  
Organic cation transporter 2  
Organic cation transporter N1  
Organic cation transporter N2  
Ornithine decarboxylase  
Osteocalcin  
Osteopontin  
Osteoprotegerin (TRAIL/Apo2L receptor)  
OTK27  
OX40 ligand  
Oxygen regulated protein 150  
Oxysterol-binding protein (OSBP)  
Oxytocin receptor  
p190-B (p190-B)  
P311 HUM (3.1)  
p53  
p55CDC  
p70 ribosomal protein S6 kinase alpha-1  
Pancreatitis-associated protein  
PAPS synthetase  
PBX2 mRNA  
P-cadherin  
PCDH7 (BH-Pcdh)c  
PDGF associated protein  
PEG3  
Perlecan  
Peroxisomal 3-ketoacyl-CoA thiolase 1

Peroxisomal 3-ketoacyl-CoA thiolase 2  
Peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase  
Peroxisomal fatty acyl-CoA oxidase  
Peroxisome assembly factor 1  
Peroxisome assembly factor 2  
Peroxisome biogenesis disorder protein-1  
Peroxisome biogenesis disorder protein-11  
Peroxisome biogenesis disorder protein-4  
Peroxisome hydratase  
Peroxisome proliferator activated receptor alpha  
Peroxisome proliferator activated receptor gamma  
Phenol sulfotransferase  
Phenylalanine hydroxylase  
Phosphatase 2A B56-alpha (PP2A)  
Phosphoenolpyruvate carboxykinase  
Phosphoglyceride kinase  
Phospholipase A2  
Phosphomannomutase (PMM2)  
Pim1 proto-oncogene  
Plasma cell membrane glycoprotein  
plasma gelsolin  
Plasminogen activator inhibitor 2  
Platelet derived growth factor B  
Platelet/endothelial cell adhesion molecule-1  
Poly(ADP-ribose) polymerase  
polyA binding protein  
Presenilin-1  
Prion protein (PrP)  
pro-cathepsin L (major excreted protein MEP)  
Progesterone receptor  
Prohibitin  
Prolidase  
Proliferating cell nuclear antigen gene  
Proliferation-associated gene A (natural killer-enhancing factor A)  
prolyl 4-hydroxylase beta subunit (EC 1.14.11.2)  
(procollagen-L-proline, 2-oxoglutarate:oxygen oxidoreductase, 4-hydroxylating)  
Prostacyclin-stimulating factor (IGFBP-7)  
Prostaglandin H synthase  
Prostate-specific antigen  
protein disulfide isomerase  
Protein kinase C alpha  
Protein tyrosine phosphatase alpha  
Protein-tyrosine phosphatase

Psoriasin 1 (S100 calcium-binding protein A7)  
PTEN/MMAC1  
Putative cyclin G1 interacting protein  
Quinone reductase (zeta-crystallin)  
RAD  
RAD 51 homologue  
RANTES  
RAP1A (ras-related protein)  
Recombination activating gene 1 (RAG-1)  
Ref-1  
RelB  
Replication factor C, 40-kDa subunit (A1)  
Replication protein A (70 kDa subunit)  
Retinoblastoma  
Retinoblastoma related protein (P107)  
Retinoic acid receptor beta  
Retinoic acid receptor gamma-1  
Retinoid X receptor alpha  
Retinoid X receptor beta  
Retinoid X receptor gamma  
Ribonucleotide reductase M1 subunit  
Ribosomal protein L13A  
Ribosomal protein L34 (RPL34)  
Ribosomal protein L37a (RPL37A)  
ribosomal protein S12  
Ribosomal protein S4 (RPS4X) isoform  
Ribosomal protein S9  
RNA-dependent helicase  
SAA-3  
S-adenosylmethionine synthetase  
Sarcoplasmic reticulum calcium ATPase  
Sarcosin  
Sec23B isoform, 2450bp  
Senescence marker protein-30  
Serine kinase  
Serum amyloid A1  
Serum amyloid A2-alpha  
Serum response factor  
Silencer of death domains (SODD)  
Small proline-rich protein (sprl)  
SMT3A protein  
SMT3B protein  
snRNP polypeptide B  
Sodium/bile acid cotransporter  
Sonic hedgehog gene  
Sorbitol Dehydrogenase  
SoxS

SPARC (secreted protein acidic and rich in cysteine)  
Spermidine/spermine N1-acetyltransferase (SSAT)  
Sphingomyelinase (neutral)  
STAT 1  
STAT 2  
STAT 3  
Stem cell factor  
Steroid hormone receptor Ner-I  
Sterol carrier protein 2  
Sterol regulatory element binding protein-2  
Stromelysin-1  
Superoxide Dismutase Cu/Zn  
Superoxide dismutase Mn  
Suppressor of cytokine signaling 1 (SOCS-1)  
Suppressor of cytokine signaling 3 (SOCS-3)  
Survivin  
Synapsin I  
Synaptophysin II  
Synaptotagmin I  
Syntaxin 3  
Tau protein  
T-cell activation gene 3  
T-cell cyclophilin  
T-cell mRNA for glycyl tRNA synthetase  
T-cell receptor  
Tenascin  
Thiol-specific antioxidant protein mRNA  
Thiopurine methyltransferase  
Thioredoxin  
Thrombin receptor (PAR-1)  
Thrombomodulin  
Thrombospondin 2  
Thymidine kinase  
Thymidylate synthase  
Thymosin beta-10  
Tight junction protein Zo-1  
Tissue factor  
Tissue factor pathway inhibitor  
Tissue inhibitor of metalloproteinases-1  
Tissue inhibitor of metalloproteinases-3  
Tissue transglutaminase  
TNF receptor-1 associated protein (TRADD)  
transcription elongation factor S-II, hS-II-T1  
Transcription factor IID  
transcriptional activator hSNF2b

Transferrin  
Transferrin receptor  
Transforming growth factor-beta 3  
Transthyretin  
Tropoelastin  
Tryptophan hydroxylase  
Tryptophanyl-tRNA synthetase  
ts11 gene encoding a G-1 progression protein  
Tumor necrosis factor associated factor 2  
(TRAF2)  
Tumor necrosis factor receptor 1  
Tumor necrosis factor receptor 2  
Tumor necrosis factor receptor-1 associated  
protein (TRADD)  
Tumor necrosis factor-alpha  
Tumor necrosis factor-beta  
Type 1 interstitial collagenase  
Tyrosine aminotransferase  
Tyrosine hydroxylase  
Tyrosine protein kinase receptor (UFO)  
U1 small nuclear RNP-specific C protein  
Ubiquitin  
Ubiquitin conjugating enzyme (Rad 6 homologue)  
Ubiquitin conjugating enzyme G2 (UBE2G2)  
Ubiquitin-homology domain protein PIC1  
UDP-glucuronosyltransferase 2  
UDP-glucuronosyltransferase 2B  
Uncoupling protein 1  
Uncoupling protein 2  
Uncoupling protein 3  
Urate oxidase  
Urokinase plasminogen activator receptor  
(uPAR)  
UV excision repair protein RAD 23 (XP-C)  
Vascular cell adhesion molecule 1 (VCAM-1)  
Vascular endothelial growth factor  
Vascular endothelial growth factor D  
Vascular endothelial growth factor receptor 1 (flt-  
1)  
Very long-chain acyl-CoA dehydrogenase  
Vesicle-associated membrane protein-2 (VAMP-  
2)  
Vesicular acetylcholine transporter (VACHT)  
Vesicular monoamine transporter (VMAT)  
Vimentin  
Visinin-like peptide 1 homolog  
Vitellogenin

Waf1

Wnt-13 mRNA

X13694

Zinc finger protein ZNF134

Zinc finger protein

Zinc-finger DNA-binding motifs (IA-1)

Zinc-finger protein-37

Zipper protein kinase (ZPK)

Serum paraoxonase

5

TABLE 5

<b>Renal Toxicity</b>	<b>Neural Toxicity</b>
Alpha-2 microglobulin	Acid ceramidase
Bile salt export pump (sister of p-glycoprotein)	Ataxia telangiectasia
Calbindin-D (28kDa)	Brain-derived neurotrophic factor
Calbindin-D (9K)	Brain-derived neurotrophic factor
Calcineurin-B	Choline kinase
Calnexin	Cystic fibrosis transmembrane conductance regulator
Cholesterol esterase	Dopamine beta-hydroxylase
endothelin-1	Dopamine receptor D2
FGF-1	Dopamine transporter
FGF-7	Endothelin-1
Gamma glutamylcysteinyl synthetase	Glial fibrillary acidic protein
Gamma-glutamyl hydrolase precursor	Glutamine synthetase
Gamma-glutamyl transpeptidase	Myelin basic protein
Heat shock protein 90	Nerve growth factor
Kidney injury molecule-1	Nerve growth factor receptor
NMB	Neural cell adhesion molecule
Organic anion transporter 1	Neuropathy target esterase
Organic cation transporter 1	Synapsin I
p-glycoprotein (MDR-1)	Synaptophysin
Phosphoenolpyruvate carboxykinase	Synaptotagmin I
Sphingomyelinase, neutral	Tau protein
Vimentin	Vesicular acetylcholine transporter
MOAT-B (MRP/organic anion transporter)	Vesicular monoamine transporter
Organic anion transporter 1	Norepinephrine transporter
Organic anion transporter 3	Serotonin N-acetyltransferase
Organic anion transporter K1	Serotonin transporter (SERT)
Organic anion transporting polypeptide 1	Sphingomyelinase (neutral)
Organic cation transporter 1	
Organic cation transporter 2	
Organic cation transporter 3	
Osteopontin	
Renal organic anion transporter	

Hepatic Toxicity	Immunotoxicity
11-beta hydroxysteroid dehydrogenase type II	
12-lipoxygenase	6-C-kine
15-hydroxyprostaglandin dehydrogenase	Complement component C3
17-beta hydroxysteroid dehydrogenase	Cyclooxygenase 2
25-hydroxyvitamin D3-1 alpha-hydroxylase	Eosinophil-derived neurotoxin
Alanine aminotransferase	Eotaxin
Alcohol dehydrogenase 1	Granulocyte-macrophage colony-stimulating factor
All Cytochrome P450 genes	IkB-a
Alpha 1-antitrypsin	Interferon gamma
Bile salt export pump (sister of p-glycoprotein)	Interferon inducible protein 10
Bilirubin UDP-glucuronosyltransferase isozyme 1	Interferon inducible protein 15
Biliverdin reductase	Interferon stimulatory gene factor-3
Branched chain acyl-CoA oxidase	Interleukin-1 alpha
Canalicular multispecific organic anion transporter	Interleukin-1 beta
Carnitine palmitoyl-CoA transferase	Interleukin-10
Catechol-O-methyltransferase	Interleukin-12
Cholesterol esterase	Interleukin-13
Corticosteroid binding globulin	Interleukin-18
Enoyl CoA hydratase	Interleukin-2
Epoxide hydrolase	Interleukin-8
Fatty acid synthase	Interleukin-4
Fatty acyl-CoA oxidase	Interleukin-5
Fatty acyl-CoA synthetase	Interleukin-6
Flavin containing monooxygenase 1	Macrophage inflammatory protein-1 alpha
Focal adhesion kinase (pp125FAK)	Macrophage inflammatory protein-1 beta
Gamma glutamylcysteinyl synthetase	Macrophage inflammatory protein-2 alpha
Gamma-glutamyl hydrolase precursor	Macrophage inflammatory protein-2 beta
Gamma-glutamyl transpeptidase	Macrophage inflammatory protein-3 alpha
Glucose-regulated protein 58	Macrophage inflammatory protein-3 beta
Glutamic-oxaloacetic transaminase	Macrophage metalloelastase
Glutamic-pyruvic transaminase	MHC class 1
Glutathione S-transferase Ya	MHC class 2
Hepatic lipase	MHC class 2 transactivator
Hepatocyte growth factor	Monocyte chemotactic protein receptor (CCR2)
Hepatocyte growth factor receptor	Monocyte chemotactic protein-1
Hydroxysteroid sulfotransferase a	Neutrophil elastase
Na/taurocholate cotransporting polypeptide	Phospholipase A2

Senescence-marker protein-30	Suppressor of cytokine signaling 1
Hepatocyte growth factor activator	Suppressor of cytokine signaling 3
Lipopolysaccharide binding protein	T-cell activation gene 3
Liver fatty acid binding protein	T-cell cyclophilin
Major acute phase protein alpha-1	
NADPH cytochrome P450 reductase	
Peroxisomal 3-ketoacyl-CoA thiolase 1	
Peroxisomal 3-ketoacyl-CoA thiolase 2	
Peroxisomal acyl-CoA oxidase	
Peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase	
Peroxisomal fatty acyl-CoA oxidase	
Peroxisome assembly factor 1	
Peroxisome assembly factor 2	
Peroxisome biogenesis disorder protein-1	
Peroxisome biogenesis disorder protein-11	
Peroxisome biogenesis disorder protein-4	
Peroxisome hydratase	
Peroxisome proliferator activated receptor alpha	
Peroxisome proliferator activated receptor gamma	
Serum amyloid A1	
Serum amyloid A2-alpha	
Transthyretin	

Cardiotoxicity	Pulmonary Toxicity
Adrenomedullin	GARG-16
Atrial natriuretic factor	GAS-7
Endothelin-1	IRF-7
Glucose transporter 1	ISG-15
Nitric oxide synthase-1, inducible	Lipocalin
Osteopontin	Liposin
Protein kinase C - beta 1	Macrostatin
RhoA	MME
Sarcoplasmic reticulum calcium ATPase	MRP14
Vascular endothelial growth factor	MRP-8 Osteopontin SAA-1 SAA-3 Tenascin Tropoelastin

TABLE 6

Apoptosis	Cell Cycle
Adenine nucleotide translocator 1	Activating transcription factor 2
Annexin V	Ataxia telangiectasia
BAK	c-myc
Bax (alpha)	Cell division cycle protein 2
Bcl-xL	Cell division cycle protein 20
c-myc	Cell division cycle protein 25
Calcineurin-B	Checkpoint kinase-1
Calprotectin	Cyclin D1
Caspase 1	Cyclin dependent kinase 1
Caspase 2	Cyclin dependent kinase 4
Caspase 3	Cyclin dependent kinase inhibitor 1A
Caspase 4	Cyclin E
Caspase 6	Cyclin G
Caspase 7	Cyclin-dependent kinase 4 inhibitor B (P15)
Caspase 8	Cyclin-dependent kinase 4 inhibitor B (P16)
Clusterin	Cyclin-dependent kinase 4 inhibitor P27kip1
Cyclin dependent kinase inhibitor 1A	Dihydrofolate reductase
Cyclin-dependent kinase 4 inhibitor P27kip1	DNA binding protein inhibitor ID2
Dynein light chain 1	E2F-1
E2F-1	GOS24 (zinc finger transcriptional regulator)
Fas antigen	MDM-2
Fas associated death domain (FADD)	p53
Fas ligand	p55CDC
Gadd153	Retinoblastoma
Interleukin-12	T-cell cyclophilin
p53	Transcription factor IID
Retinoblastoma	Ubiquitin-homology domain protein PIC1
Thymosin beta-10	Waf1
Tumor necrosis factor receptor 1	
Tumor necrosis factor receptor-1 associated protein (TRADD)	
Waf1	

Cell Proliferation	DNA Damage
Activin beta E	Activating transcription factor 2
Activin receptor type II	Ataxia telangiectasia
c-abl	ATP-dependent helicase II (70kDa)
c-erb A-1	ATP-dependent helicase II (Ku80)
c-fos	BRCA1
c-jun	c-abl
c-myc	Cell division cycle protein 20
Early growth regulated protein 1	Checkpoint kinase-1
Endothelin-1	Cyclin D1
Extracellular-signal-regulated kinase 1	Cyclin-dependent kinase 4 inhibitor B (P16)
FosB	DNA dependent protein kinase
GOS24 (zinc finger transcriptional regulator)	DNA ligase I
GT mismatch binding protein	DNA ligase IV
Hepatocyte growth factor receptor ID-1	DNA polymerase beta
Insulin-like growth factor II	DNA repair and recombination homologue (RAD 52)
Interleukin-6	DNA repair protein (RAD 50)
L-myc	DNA topoisomerase I
MutS homologue (MSH2)	DNA topoisomerase II
Proliferating cell nuclear antigen gene	Dynein light chain 1
Replication protein A (70 kDa subunit)	ERCC 1 (excision repair protein)
Ribosomal protein L13A	ERCC 3 (DNA repair helicase II)
Thrombospondin 2	ERCC 5 (excision repair protein)
Thymidine kinase	ERCC 6 (excision repair protein)
Thymidylate synthase	FEN-1 (endonuclease)
Transforming growth factor-beta3	Gadd153
	Gadd45
	GT mismatch binding protein
	JNK1 stress activated protein kinase
	L-myc
	MDM-2
	MutS homologue (MSH2)
	Nucleoside diphosphate kinase beta isoform
	O-6-alkylguanine-DNA-alkyltransferase
	p53
	p55CDC
	Poly(ADP-ribose) polymerase
	Proliferating cell nuclear antigen gene
	RAD 51 homologue
	Ref-1

|  
| Replication protein A (70 kDa subunit)  
| Retinoblastoma  
| Transcription factor IID  
| Ubiquitin conjugating enzyme (RAD 6  
| homologue)  
| UV excision repair protein RAD 23 (XP-C)  
| Waf1

Inflammation	Peroxisome Proliferation
12-lipoxygenase	17-beta hydroxysteroid dehydrogenase
Apolipoprotein AI	Apolipoprotein CIII
C-reactive protein	Bilirubin UDP-glucuronosyltransferase isozyme 1
Calprotectin	Branched chain acyl-CoA oxidase
Cyclooxygenase 2	Carnitine palmitoyl-CoA transferase
Fas ligand	Cytochrome P450 4A
IkB-a	Cytochrome P450 4A1
Intercellular adhesion molecule-1	Enoyl CoA hydratase
Interleukin-1 alpha	Epoxide hydrolase
JNK1 stress activated protein kinase	Farnesol receptor
NF-kappaB (p65)	Fatty acyl-CoA oxidase
Nitric oxide synthase-1, inducible	Glucose-regulated protein 58
Phospholipase A2	GOS24 (zinc finger transcriptional regulator)
Serum amyloid A1	Hepatic lipase
Serum amyloid A2-alpha	Lipoprotein lipase
Tumor necrosis factor associated factor 2 (TRAF2)	Liver fatty acid binding protein
Tumor necrosis factor receptor 1	Malic enzyme
Tumor necrosis factor receptor 2	Peroxisomal 3-ketoacyl-CoA thiolase 1
	Peroxisomal acyl-CoA oxidase
	Peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase
	Peroxisome assembly factor 1
	Peroxisome assembly factor 2
	Peroxisome biogenesis disorder protein-1
	Peroxisome proliferator activated receptor alpha
	Peroxisome proliferator activated receptor gamma
	Retinoid X receptor alpha
	Uncoupling protein 1
	Uncoupling protein 2
	Uncoupling protein 3
	Urate oxidase
	Very long-chain acyl-CoA dehydrogenase

TABLE 7

1-chloro-2-nitrobenzene	dt-5-fluorouracil
2,4-dinitrophenol	erythromycin
2-acetylaminofluorene	ethyl methanesulfonate
2-azido-2-deoxycytidine	etoposide
2-azido-2-deoxyuridine	fenofibrate
4-acetamidofluorene	flufenamic acid
5-azacytidine	gemfibrozil
5-chlorouracil	guanine
5-fluorouracil	hdp527
6-mercaptopurine	hydroxyurea
6-thioguanine	icrf
acetamidofluorene	icrf/doxorubicin
acetaminophen	indomethacin
acetylsalicylic acid	iodoacetamide
acridine	isonicotinic acid
actinomycin	M077
allyl alcohol	mechllorethamine
aminopterin	melatonin
aminotriazole	melphalan
antimycin a	methotrexate
antipyrine	methyl methanesulfonate
benz[a]pyrene	mitomycin c
bleomycin	mitoxantrone
busulfan	n-nitroso-n-ethylurea
caffeine	n-nitroso-n-methylurea
camptothecin	naloxone
carbamazepine	naproxen
carbon tetrachloride	nicotine
carboplatin	nitrofurantoin
carmustine	o-toluidine
chlorambucil	oligomycin
chloroquine	paclitaxel
cimetidine	PGU693
cisplatin	phenobarbital
clenbuterol	phorbol 12-myristate 13-acetate diester
clofibrate	prednisone
clozapine	proflavin
colchicine	progesterone
corticosterone	puromycin
cycloheximide	rezulin
cyclophosphamide	rifampicin
cyclosporin	rosiglitazone
cytosine arabinoside	sodium azide
dacarbazine	streptozotocin

dexamethasone  
diethylhexylphthalate  
diethylstilbestrol  
diflunisol  
digitoxin  
dimethylhydrazine  
dmso  
doxorubicin

tacrine  
tamoxifen  
thioguanine  
transplatin  
triethylenemelamine  
triethylenethiophosphoramide  
verapamil  
wy 14,643

**TABLE 8**

1	Activating transcription factor 4
2	Activin receptor type II
3	Ataxia telangiectasia
4	c-H-ras
5	c-jun
6	Carnitine palmitoyl-CoA transferase
7	complement component C3
8	Cytochrome P450 1A1
9	DNA dependent helicase
10	DNA mismatch repair protein (PMS2)
11	Epoxide hydrolase
12	ERCC 5 (excision repair protein)
13	ERCC 6 (excision repair protein)
14	Farnesol receptor
15	Gadd45
16	Glucose-6-phosphate dehydrogenase
17	Glutathione peroxidase
18	Histone 2B
19	Interleukin-1 alpha
20	Interleukin-6

**TABLE 9**

<b>CELL TYPES IN THE HEART:</b> Myocytes (cardiac muscle cells) Vascular endothelial cells Purkinje cells - regulate rate and rhythm of the heart
<b>CELL TYPES IN THE LUNG:</b> Columnar, ciliated epithelial cells - line trachea, bronchi, bronchioles Goblet cells - secrete mucus Neuroendocrine cells - contain serotonin, calcitonin and gastrin-releasing peptide Capillary endothelial cells Interstitial fibroblast cells Smooth muscle cells Mast cells - in pulmonary interstitium Type I alveolar (epithelial) cells - compose 90% of alveolar surface Type II alveolar (epithelial) cells - secrete surfactant and mediate repair of alveolar epithelium Alveolar macrophages Serous cells - produce a fluid to dissolve mucus Brush cells (Type III epithelial cells) Clara cells - highly metabolic Parenchymal cells (connective tissue cells)
<b>CELL TYPES IN THE KIDNEY:</b> Capillary endothelial cells Visceral epithelial cells (podocytes) - form glomerular barrier Parietal epithelial cells - line Bowman's space Mesangial cells - have contractile abilities to reduce amount of glomerular surface available for filtration Tubular epithelial cells Juxtaglomerular cells (modified granulated smooth muscle cells; also called granular cells) Lacis cells (non-granular cells) Fibroblast-like cells Macula densa cells (specialized tubular epithelial cells)
<b>CELL TYPES IN THE BRAIN:</b> Neurons Astrocytes - found in gray and white matter; responsible for repair and scar formation Oligodendrocytes - main component of white matter; produce and maintain CNS myelin Microglia cells - serve as macrophage-type cells Ependyma cells (columnar epithelial-like cells with a ciliated border) - line the ventricular system Fibroblasts Capillary endothelial cells Meningeal fibroblast cells Leptomeningeal (mesenchymal) cells Purkinje cells Meningothelial cells

**Macrophages****CELL TYPES IN THE LIVER:**

Kupfer cells - resident macrophages

Sinusoidal endothelial cells

Ito cells (lipocytes) - synthesize collagen and store vitamin A

Hepatocytes (parenchymal cells) - majority of cells in the liver are of this type

Bile duct epithelial cells

Hepatic venule endothelial cells

Sinusoidal epithelial cells

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
1	A + AP8	Inhibitor of apoptosis protein-1	310bp	<pre> AAGCTTTACCGCTGAGAATGATGA GGATGAGAAATGGGTGAGGTT ACATTAGAATGAAATGAGGAAACTTA GAAAATTAAATAAGACAGTGATG AATACAGAAAGATTTTATAACAA TGTGTAATGGAGTTAGATAACAATT CTTACCTTTGAGGGAAATAATTGTT GGTAATGAGATGTGATGTTCTCT GCCACCTGGAAACAAAGCATTGAA GTCTGCAGTTGAAAAGCCCAACGT CTGTGAGATCCAGGAAACCATGCT TGCAAACCATGTT </pre>	Repressed in Individual 1 and constitutive in Individual 2	AF070674
2	A + AP7	No significant match to anything	200bp	<pre> AAGCTTAACGAGGAAATAATATCAG TTAAATTTAGTTGACATTGTTA GGAACCAAGGTTAACAAATGAN AAAAAAAGCAGGGTGGGTGGTTCT GTGCCTGTAATCCCAACACTTGG AAGGCTGAGGTGGAGGATCACTT GAGCTCAGGAGTTGAGACCAACCT TGGAACATAGCCAGACACTCACT CTACT </pre>	Repressed in Individual 1 and constitutive in Individual 2	
3	A + AP5	Gu protein (nucleolar RNA helicase recognized by autoimmune antibodies from a patient with watermelon stomach disease)	124bp	<pre> ACATACTCTTGAGCAATGCTAATCT GCGCCCTTACTCCCTAAGTCCT CTTGGTAATAATGTTAATCTTC AATAGGAAGGAAGTGGAGTACATTA CCATTTAAGGCCATTATCCAGGC TACTAAGCTT </pre>	Repressed in Individual 1 and constitutive in Individual 2	AF261917

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
4	A + AP7	Ribosomal protein L34	117bp (65bp match)	GGAAGCTTAACGAGGAGCAGAAA TCGTTGTGAAAGTGTGAAGGCAC AAGCACAGACTGAGCTAAAT AAAAAAATGAAACCTTTTGAGTAA TAAAAATGAAAAAGACGCTGT	Repressed in Individual 1 and constitutive in Individual 2	NM_000995
5	G + AP5	clone 459L4 on chromosome 6p22.3-24.1	171bp	AAGCTTAGTAGGGCAAAATAGGGTTGT TGATGATGAAAGTGGTTGTGTTTA TAAGAGTCCTTAGGCTCTAGATGG CATTTGAACCTGGGTTCCAGTGAT TACCAAGAACCCCTGAATTGAAGAAT ACATGCTGTGGCCCTTCAGCTCA GAAACTTTTACTTTCTATTGCGC	Repressed in Individual 1 and constitutive in Individual 2	AL031120
6	C + AP6	eukaryotic translation initiation factor 3 (subunit 10 -theta)	126bp (86bp match)	AAGCTTGACCATATGCCATCCACGGAG GTTGGAAAAAACCATGCCATTTCTG GAATTAAAGGGTGTGCATTATTTC ATCAATCATTTGTGACAAAAAGA AAAACATAAAAATAAAATTAAAATGT G	Repressed in Individual 1 and constitutive in Individual 2	NM_003750
7	G + AP7	ribosomal protein S9	94bp (86 bp match)	GTAAGCGCTGATCCGTATTG GCAGGGAAACGAGACAATCCAGCA GCCAGGGAGCAGGGACTT ATCCCTCCCTCGTTAGCTT	Induced in Individual 1 and Individual 2	NM_001013
8	C + AP6	No significant match to anything	182bp	AAGCTTGACCATATGTGATTAACGTA TCATCCCCTGCTCACCCACAATGTT CGTTCCCTGCTCACCCACAATGTT GGCTTCATAGACTCAAGTGAAG GGGCACTTTATAATTGGCTGAAGA ATTCCCTTAGAACGCCTAAGAGATTA AGACCACAGGATGCTCAAAGGTC TTCTTTCTTG	Repressed in Individual 1 and constitutive in Individual 2	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
9	C + AP7	No significant match to anything	98bp	CCAAGATGCCGGCACTGCACGG CTTTATCAGTTTATTACATCAG GTCAAGAACAAATGGAATCTATC CACATGGTCTGCCCTGTTAAGCT	Absent in Individual 1 and repressed in Individual 2	
10	G + AP6	KIAA1225 protein	252bp	AAGCTTAGTAGGGAGCACTTTAAA ATATGTGAACCTCAAATATTGCACT TCTTCAGATGTTATCAATTGGTT ATTGTAATGTTACTCATTTAGTTGA TGTAATTTAACCTTTAACAACTCTT TGATTGAAACCCCTTAAAGGAAATT TTTCAGTACTATTACATAGGAATT GATTTTATGGATAATGTTAGAAGAA ATGTGCTGTATTGATAAAATTCA CTTATTGTATGTGTGTTAATCT	Constitutive in Individual 1 and repressed in Individual 2	AB033051
11	A + AP5	erbB2-interacting protein ERBIN (KIAA1225 protein)	252bp	AGATTACAACACATACAATAAGT GAATTTTATCAAATACAGCACATT TCTCTACTATATCCATAAAAATCAA TTCTATGTAATAGTACTGAAAAAT CAAATAAAATGAGTTAAAATTACA AAAGAGTTGTTAAAGGGTTCAATCA AAATTAAAACATAACAGTACAAT ACCAATTGATAACATCTGAAAGA AGTCAATATTGAGTTCACATATT TTTAAAAGTGTGCTACTAAGCTT	Repressed in Individual 1 and constitutive in Individual 2	NM_018695
12	G + AP7	angiotensin II receptor (AGTR1)	76bp	AAGCTTAACGAGGCTATCAGCAA CAAAGAGAACAGGGCCAGGTGG CTCAATAGCCAGGTACAAATGGT TGCCCC	Repressed in Individual 1 and induced in Individual 2	AF245699
13						

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
14	C + AP11	Alpha-enolase	153bp	AAGCTTCGGTAAATGGCCCAAGT CATTGTTTCTCGCTCACTTCC ACCAAGTGTCTAGAGTCATGTGAG CCTCGTGTATCTCGGGGTGGCC ACAGGGCTAGATCCCCGGTGGTTT GTGCTCAAAATAAAAGCCTCAGT GAACCCATG	Constitutively high in Individual 2 and induced in Individual 1	AF035286
14	C + AP11	Calmodulin 3	152bp	CAGGTAGTCACTGTATTTATTGGA AAACATTGATATATATTTCCTCAC AGCTTGAACTGAACACAATATTGCC CGGTTAAAAAACAAAACCAAAA CATTCGAAAATGTCCACAGGCCTC ACGCCCTACCTGCCCTACCCGAAAG CTT	Constitutively high in Individual 2 and induced in Individual 1	NM_005184
15						
16						
17						
18	A + AP19	No significant match to anything	91bp	AAGCTTATCGCTCCCACTCCAGAG AAACTTAAATGCTCAGGCTCAAAC TCCCCTATCTCCCTCAGGGT CCTTCTGTCCTCTTACT	Repressed in Individual 2, but not in Individual 1	
19						
20	A + AP19	Clone RG013F03	126bp (93 match)	AAGCTTATCGCTCGCAGGGGTTC CGTAGTTCTCTCGAGGCCAATGCA TGTTATTAGCAGCAGGTGCTTTG TGCTTCTCATAGTAACGTACT ACITGTAATAACATTTCTATTTC	Absent in Individual 2 and induced in Individual 1	AC005046

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
21	A + AP23	clone 1189B24 on chromosome Xq25-26.3.	289bp	ACTCTGAAGATCTGTTAACATGATGATGAAATTATTCCTCCCCAATCAAGAAATTACATGACTTTAAAAAACATCATCCAGTATGACCGGAAGTTGATAATCAGAAGTGGTAACTCTCACCGCCGTGGAAACATGATCGCATAATCTCCCTCTGAAAGATAAACTTCAACAGTAAACATTTAAAGTCTTCAGAATCCTTCTGTCAATCTAGTCTGTAAATCACATTTAAATAATTGGTACCCCATAGCCAAAGCTT	Repressed in Individual 1 and constitutive in Individual 2	AL030946
22	C + AP22	Interferon, gamma-inducible protein 16	135 (71 match)	AAGCTTTGATCCATGGAAATGGGTATTGGAGGTGCTTTTAATTTTCATAGTTTTTTAATAAAATGCCATTTGCATCTACAACCTCTATAATTGGAAAAATAAAATAACATTATCTTTTGTT	Constitutive in Individual 2 and repressed in Individual 1	AF208043
23	C+AP17	Kinectin 1 (kinin receptor)	183bp	AAAGCTTACCAAGGTGTTAGAGTGAAGTAATTGGGAAACTGTTCAATTGAGATAAAAAAGGCATTGTTATTATTTGGCCAAATTAAAGCCTTATTATTTTCACCCCTTCTACTTTGTCTGAAACACTGAACAGAGTTTGCTTTCTAATCCCTGTTAGACTACTGATTAAAGAAGG	Constitutive in Individual 1 and repressed in Individual 2	NM_004986
24						
25	C + AP 24	KIAA0911 protein	119bp	CCAAACTAGTGCATGTATAAATGGCAGGATGGGGTACTGTGATGATTAAACTGACTTTTAATTTTGTAATAAAATCGGATTCCCTGTGT	Constitutive in Individual 2 and induced in Individual 1	NM_014944

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
26	G + AP28	No insert - just vector sequence				
27						
28						
29						
30						
31	C + AP26	No insert - just vector sequence				
32	A + AP28	Ribosomal protein S12	80bp	ACATCACAGGCCAGGGTCTGTT TATTAACACCCCTCCAGCAGAG GGCAGTACAGTGCTGTCCCAGC AGAAGCTT	Repressed in Individual 2 and constitutive in Individual 1	AF058761
33	C + AP27	KIAA0890 protein	69bp	CACAAGGGATAATAGAACTTTATT TTAAATAAACATTTGCACCTGTAC ACAGCCCCAGCAGAAAGCTT	Induced in Individual 3, but not in Individual 4	NM_014966
34	C + AP29	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit e (ATP51)	149bp	CACACAACACAGGAAGGCCTTATTCA TCGGCTGTGGTCCAAGAGTGGG TCGCAGGGTCACTCACTTTAAATAG CTGTCATCTCTGCCAAATTCTCTGG CAATCCGTTTCAGTTCATCCTGCTT CTTCTCTCTGCTGCTAAGCTT	Repressed in Individual 3, but not in Individual 4	NM_007100
35	G + AP31	carbonyl reductase	175bp	GGCAGCGAATCAGGGTTATTGG AGGGATTGGGGTAGGGATGAGCAC GGCATGGGGCTTGAGGTGTGG AGGGAGCTCAGCAGGCCAGAAG CCCCCTCACCAGAAAGTGGAA CCGGTGGTCACTGCCACTTGGTCA CTCAGCAGAAAGAGGATGGCTTC ACCAAGCTT	Slightly induced in Individual 4, but not in Individual 3	NM_016286
36						

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
37	A + AP10	KIAA1224 protein	223bp	ACAGGTTCATCTGAATACATATT ATTAGATAAAATTAGGGTTGTCA CATCATCTAACATACATACAGCTTG CAAGACTAGAAAATCACAAATTAGTTT TTTGACCAGTTAAAGTATGAAATG ATTGCATTGTACATACGATGTACAA AGACCGATGATGGTTCTGTGGGAG TTACTTCAGGCTGCACTGGTGGGT GTGTTATGTGTGTACGGTGGAAAGC GCAAGTNCAGGGTNACCTTATTG ACCCCCAGCTGGCACTGNTNGNC CCCTACATCAATTACCCGGAAAGCTT GANATTGAAATGGTTATAAACTCT GTCTTCGTGAGCTGGATGGCAAGC TCTCACACTTACCCGAAGCTT	Reduced in Individual 4 and constitutive in Individual 3	AB033050
38	G + AP11	CAMPATH-1 (CDw52) antigen	71bp	ACCCCAGCTGGCACTGNTNGNC CCCTACATCAATTACCCGGAAAGCTT GANATTGAAATGGTTATAAACTCT GTCTTCGTGAGCTGGATGGCAAGC TCTCACACTTACCCGAAGCTT	Induced in Individual 4, constitutive in Individual 3	X62466
38	G + AP11	tumor necrosis factor type 2 receptor associated protein (TRAP3)	71bp	ACCCCAGCTGGCACTGNTNGNC CCCTACATCAATTACCCGGAAAGCTT GANATTGAAATGGTTATAAACTCT GTCTTCGTGAGCTGGATGGCAAGC TCTCACACTTACCCGAAGCTT	Induced in Individual 4, constitutive in Individual 3	NM_021138
39						
40	G + AP10	Insert size doesn't match the autorad	54bp	AAGCTTCCACGTAACCAACAGCCCC AAATCCATGATAAAAGCTTCCACGTA CTTACCC	Repressed in Individual 4, constitutive in Individual 3	
41	C + AP9	Sperm autoantigenic protein 17 (SPA17)	216bp (126 match0	CACAAACAGTAACGAAATGTTATTCA CAACATCAAATCTTCCTTCAGG AAGAAAATGACATTAATAAGAAAGGT GATGGGATTGGATTATTTCATGT TTCTCTGGAGGTAAAACCACTGTGCC TCACCTGGTTTCCTCTTCCTCAT TTGAAGAAGCTATTGTTTCATGTGTC TTTGCCCTCCCTCTGGCTATGTGTC CCCGGAATGAAAGCTT	Constitutive in Individual 3 and repressed in Individual 4	NM_017425
42	C + AP10	No insert - just vector sequence				

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
43	C+AP16	A kinase anchor protein 2 (PRKA2)	30 bp (matches 19)	CAATTATTGCCGCTCTAAAGCTTCC TGAAAT	Constitutive in Individual 4 and repressed in Individual 3	NM_007203
44	G + AP23	growth arrest specific transcript 5 gene	314bp	AAGCTTGGCTATGGAGAGTCGGCT TGACTACACTGTGGAGGCAAGTT TTAAGGAAGCAAAGGAACTCGAATT CATGATTGAAGAAAATGCAGGGTTT TAATGACCACAAACAAAGCAAGCAG CAGCTTACTGCTTGAAGGGCTT GCCTCACTCCAAGCTAGAGTGCAGT GCCCTTTGAAGCTTACTACAGGCCT CAAACCTCTGGGGCTCAAGGTATCC TCAGGCCCTCCCAGTGGCTTGTAG ACTGCCTGATGGAGTCTCATGGCA CAAGAAGATTAACAGAGTGTCTCCA ATTTAAATAAATTGGCAATCC	Induced in Individual 4, but not in Individual 3	AF141346
45	G + AP19	5-aminolevulinate synthase 2 (ALAS2)	255bp	AAGCTTATCGCTCAAAGTCCTAC CCCTCTCTTCCCTTTAAAGCCCTC TCTTCCTCTGCTTTCTTCCTACCTA GCTCCTTGTGGTGAACCCAGCCCC GCCTTAACCTCTGTAACCCAGCCCC TTACACCACTTCCACCTCCCTGTC CGAAAGTACACGGACACTAGCTGCC CCAGGAAGTTGGTGTGATTTAAATC ACTCTGTCTTGGTGGAAAGTGTGTA TTTGTGATAAAATAAGTCTGTGTA TTTGTTC	Induced in Individual 4, but not in Individual 3	AF068624
46	G + AP23	Clone NH0523H20	101bp	GGGTGGAGGGGGTACCTTATGAAT ACCAAGGGACAAGGAAGGCTGC TCTTNTCACACACACTGCTGAATCTCC GGATCTCCGCAAGGTCATAGCCAA GCTT	Constitutive in Individual 3, increased in Individual 4	AC005041

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
47		Very tiny insert		GCANACCATAGGAAGTTTATTGTGT CTTGANACACTACAATGCCAGACTC CTCTCCANAGAAAGGCTTCAA GACAGGGAAACCGTCATCCGGATGC GTTGCTCATTTGTCAATTCATAGC CAAGCTT	Constitutive in Individual 3, increased in Individual 4	NM_014402
48	G + AP23	Low molecular mass ubiquinone-binding protein	131bp	AAGCTTGGCTATGATGTTGAAGAC CAATCTTAACATCTGATTATTTG ATTATTATTGGAGTGTTGGAC CATGTGTGATCAGACTGCTATCTGA ATAAAATAAGATTGTC	Repressed in Individual 3, but not in Individual 4	NM_006476
49	G + AP23	ATP synthase, H+ transporting, mitochondrial F1F0, subunit g (ATP5JG)	118bp	AAGCTTCACTANCACAATGTCCTGCC ATAAAAGTAGGCCCTGATAAAGAAAT GGACATTATCTAAATTGTCCTCATCT CTCCCACTGCTGCCCACTTCT TGCCATTCAAGCAATATANACATCTGA TCCGTTCCCTCAAGATTCTATTCTCA CCCTTCCCTAACAAAGATGACAGG	Induced in Individual 4, but not in Individual 3	S75476
50	C + AP24	phosphoglycerate kinase 1	173bp	ATATCTCTAGTTGTTTTATACT CCCCAGTTTATTTGAAATATTCTAT GATTTGACATTATCTCAAATACA CAGAAATTACCTTACATCTGCCAT ACATTATTAAATGCTGATGAAGAA TACTTTACCAATATTAAAGGATGCC AAAATAATAACACTTTCCCAACTTT AAAATTATTTAAATAAGCCAAAT TTATATTGACATTGGTTACATG TGCATAATAAAACAGTCATATTCT CAACTGACCATAGCCAAGCTT	Constitutive in Individual 3, repressed in Individual 4	NM_007099
51	A + AP23	Acid phosphatase 1	274bp			

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
52	C + AP20	Clathrin, heavy polypeptide-like 2 (CLTC2)	246bp	CCACAGTCCAGTAATTATTAAATTGAGTAATTCAAAATCCACAAA CAAAACTGAAGAACAGCAATTATTTGTTGAATTCTCTCTGTACACTAGTGATCTAAACACCACAAATATCCAACATACACAAACCTCAGGGAA GGGTTAGTAACACACACAAGATTGAATCATGGTGCTCTTGCTCCCTGAATGGAAATGGTCCCACAGAAAAAGCACAGGATAACGCACAAACAGCTT	Induced in Individual 3, repressed in Individual 4	NM_004859
53	C + AP21	MHC class II HLA-DR-beta (DR2-DQw1/DR4 DQw3)	223bp	AAGCTTCTCTGGACCTGGTTGCTA CTGGTTGGCAACTGCAGAAAAATG TCCTCCCTGGCTGGCTCCCTCAGCT CCTGCCCTGGCCCTGAAGTCCCCAG CATTGATGGCAGGCCCTCATCTTC AACTTNNGCTCCCTTGCTCAA ACCGNATGGCCTCCGGTGCATNTG TATTCAACCTGTATGACAAACACAT TACATTAAAATGTTCTCAAAGATGG	Repressed in Individual 3, but not in Individual 4	M20430
54	A + AP23	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex	250bp	AAGCTTGGCTATGGTTAAAGCGGA ACCAAGATGTTAAAAAATTAGAAGAC CAACTTCAGGGGGTCAATTAGAA GAGGTGATTCTTCAGGCTGAACAT GAACCTAAATCTGGCAAGAAAAATGA GGGAATGGAAACTATGGGAGCCAT TAGTGGAAAGAGGCCCTGGGATC AGTGGAAATGGCCAATAAATTATT AAGTGACTTTGGTGTGTTCATGG AAACTGATGTAATTAAATATTCTGTT ATATT	Constitutive in Individual 3 and repressed in Individual 4	NM_005000

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
55	C + AP19	clone 717M23 on chromosome 20	363bp	CCAAATTTCCTCAATTTCATTGAGTTA CCACCAAAGTGTAAATTAACAAT GTGATAGGGTGTACAGTAGTTT CAATTGTAACAAACATGCCTATGTTT TATATAAATTATAGCTGATCAACTA GAGAATAAAATAATTATCCTTTAT TTAGGTCTCTTTTACATTCACTGTT CTTTACAGGGTTGAAAAACAAACC TTCACACAGGAATTGACAAATCAA GGAATTGAGAAGCTCCTTACTGCC TGGTATCCATTGGCACTTGTCA CAGAAGTAGGACAGCTGCTCCTCC ATCCAAGAACAGTCTCCACTCTGT TGTTGAGGGAAATCCCACACTGT CGAGCGATAAGCTT	Induced in Individual 3 and repressed in Individual 4	AL050321
56	C + AP20	FLJ22624 fis, clone HS105951	85bp	AAGCTTGTGGCACAGGATCAAC ATGATGGTGAATGGAAAAATA CTTCNAAGTAACATGCTTAGCTTCC CTCCCTTAATGTG	Repressed in Individual 4, but not in Individual 3	AK026277
57	C + AP24	No significant match to anything	106bp	AGGGGTTTACCAAGAGCATTATT TACTCTTTAAGATACTAATGAAAGAC CCTTAATATTGGTAAATCATACA TATAGGTTACATTACAGCTAGNG AAGCTT	Induced in Individual 4, but not in Individual 3	
58	C + AP19	clone RP11-468G5	72bp	AAGCTTATCGCTCAATAGTGCATT AACAGAAAACTCTACAGGATTATA CACAGTAGTAACACTGGCCCTG	Induced in Individual 4, but not in Individual 3	AC009238
59	G + AP2	histone macroH2A1.2 (H2AF12M)	31bp	AAGCTTGCACCATGTACCCACCT TCAGTT	Increased in Individual 3, not in Individual 4	NM_004893
60						

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
61	G + AP3	KIAA0949 protein	104bp	AAGCTTAACGAGGAATGAGAACAC AAGGAATGATTCAAGATCCACCTTG AGGGAAATGAACCTTGTGTTGAAAC AATTAGTGAATAAGCAATGATCT AAAATC	Repressed in Individual 3, but induced in Individual 4	AB023168
62						
63						
64						
65						
66						
67	G + AP5	BCL2-related protein A1 (BCL2A1)	122bp	CGAGAAAAATACATACAATTATTTC ATTACATGGGGACAAAATTCCATA ACTCTGGAAGGGTCAAAGTTACATCAT CAAAGTTGTTTATTAAAAGTAGAA GTATGTGGCAATCAAGCTT	Increased in Individual 4, but not in Individual 3	NM_004049
68		Insert is too small				
69	A + AP4	No significant match to anything	139bp	CACAATTATTATTGAGCTTTGCT GTATGTAGCCTTTGAAGTAGATT TATAGTTAGAATTGTGCTTCCCT TTTTAACTCTTCACTCTTCATTTTT ATTGAGCTATGAATAACTATTGTA GCGGTAAAGCTT	Induced in Individual 4, but not in Individual 3	
70	A + AP4	chromosome 21, clone:KB51A8	123bp	AAGCTTTACCGCTACTGAGTCTGT GTAGTAATTTTGACTAGNNACAT GGTGAGATTACATTATAAAGTGTG AAGTTTGTTAAGGTTCTTAAAG AATATTACGCTTTCTGGCCGGCG	Slightly induced in Individual 3, but not in Individual 4	AP001628
71	A + AP3	No significant match to anything	110bp	AAGCTTAACGAGGGATGGCAGCTG ATGGGTACCCAGGTCCCTTATGGG ATGATGAAAAGCTCTGAAATTAGC TGTGGTGTGATAATTGCACAACTC CGTGGATATCG	Induced in Individual 4, but not in Individual 3	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
72	A + AP3	RECQL4 helicase	50bp	CCAAAGTGAGCATTTCATTCTGC ATTTGGAGGCCCTCGTTAACGCTT	Induced in Individual 3, but not in Individual 4	AB026546
73	G + AP4	Insert is too small			Induced in Individual 4, but not in Individual 3	
74						
75						
76	A + AP23	cyclin D2	179bp	AGGTCAAGGGAGTTTATTGTCA ATAGCATTAACCTAAATTGCATTCAA AACCATTTCAAATCCATCTTTAA CTAGTCANAAAACAGGGTTATTATT TTTTAAATCCTACTTANOACTGAACAG ATAAGACCTCTTAAAGGCAGGTG ACTATATCATGTCACCATCATAGCC AAGCTT	Highly induced in Individual 4, but not in Individual 3 or Individual 5	NM_001759
77	A + AP23	clone RP1-63P18 on chromosome 1	124bp	AAGCTTGGCTATGGGTTGCCTAA TTGATGTTTGAGGAAGCATATTAA TGTTATAAAACTTCGCTGACTTTGAA GGTNGTGTGTAGCATGAGGGANCA CAAATAAAACAATTCTAAATCAAAC T	Induced in Individual 4, but not in Individual 3 or Individual 5	AL356379
78	C + AP19	No significant match to anything	38bp	CTAGAAAAGCAGACACTCCATAACC TGAGGGATAAGCTT	Induced in Individual 4 and Individual 5, but not in Individual 3	
79	C + AP19	No significant match to anything	36bp	AAGCTTATCGNTCAGGTATGGAG TGTCTGCTTCT	Induced in Individual 4 and Individual 5, but not in Individual 3	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
80	C + AP24	cytochrome c oxidase subunit VIic (COX7C)	213bp	CACGTATTAAGTTTATTGACAAACA TATCTAGTATGGCATATGAGTTCTA GTTTGATCACTCCAGGGCTGC ACCTCTAAATGCTCTTCATATCT GTTAAATGGAGGAACTGAAACATC CTTATGTTTAAGCAGTTGGTGTCT TACTACAAGGAAGGGTAGCAAATG TGAGATCAAAGTACAAACATCT TAGCTAGTGAAAGCTT	Induced in Individual 3, but not in Individual 4 or Individual 5	NM_001867
81						
82	C + AP24	clone RP11-358M9	146bp	CAGTTAAAAGAAATGGTAGACAC CTATATTACTTTGTTAGACATACA AAGGCTAGCCTCTTTGACTTGTAC AAAGTTTCAAACCTTCATAACAA ATATGCCCACTCATTATTCACTCA TCGGACAGCTAGTGAAGCTT	Very high expression in Individual 4 and Individual 5, but not in Individual 3	AC020595
83	C + AP19	Human mitochondrial DNA	35bp	AAGCTTATCGCTCACACCTCATATC CTCCCTACTG	High expression in Individual 3, but not in Individual 4 or Individual 5	NC_001807
84	C + AP1	ribosomal protein L3	64bp	AAGCTTGATTGCCAGGAACAGATT TGCAAGTTGGTGGGTCTCAATAAA AGTTATTTCCACTG	Slightly induced in Individual 3, but not Individual 4 or Individual 5	M90054

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
85	C + AP8	No significant match to anything	239bp	AAGCTTTACCGCTAAATGATGAT ACANGTTGAAGACACATCACTCTG AAATTGGAAAGACCTOACCACTTAAG GCTCCACAGTGCCTACTCAGCTG AACTCTAGTTACTACTCTTTACTT TGTCACCCATNGGGGGTGCAGT TTTTTTAAAATGTTGGAGATGCC ATTCTAACTACTGTGGATGTCTCT GTTTGGGAGGGTATAACAAGAAAT AAAAAGANTATAATG	Induced in Individual 4, but not in Individual 3 or Individual 5	M35543
86	C + AP19	GTP-binding protein G25K	266bp	AAGCTTATCGCTCCAAGACTGCT GAAAAGCTGGCCGTGACCTGAAG GCTGTCAAGTATGTGAGGTGTTCT GCACCTACACAGAGGGTCTGAAG AATGTGTTGATGAGGCTATCCCTAG CTGCCCTCGAGCCTCGGAAACTC AACCCAAAAGGAAGTGTNTATT CTAAACTGTTTCTCCCTCCCTCT TTGCTGCTGCTCCGTCCCCACTA CTGNAGAAAAGATGTTAAAAACAA AGGAATAAAACCNCTGTGTTG	Induced in Individual 3, but not in Individual 4 or Individual 5	

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
87	C + AP36	ribosomal protein S4, X-linked (RPS4X)	332bp	AAGCTTCGACGGCTGGTAACCTGT TATGGTGACTGGGGTGCTAACCT AGGAAGAATTGGTGTGATCACCAA CAGAGNGAGGCACCCCTGGATCTTT TGACGTGGTTCACGTGAAAGATGC CAATGGCAACAGCTTGGCACTCG ACTTTTCCAAACATTGGTTATTGGC AAGGGCAACAAACCATGGATTCT CTTCACCCGAGGAAAGGGTATCCGC CTCACCATGGCTGAAGAGAGAGAC AAAAGACTGGGGCCAACAAAGC AGTGGGTAAAATGGGTCCCTGGGT GACATGTCAAATCTTGTACGTAAAT TAAAAATAATTGGCAAG GGTCAAGACACCTTCAGAAAAATG TTAGAAATCTACACCTACGTCA TTTCATTGGTTACAATTGGCTAA TTCAATTCTCTCTAGTATA GATCAGATCAGTGTACCTCCAAAC AGAGATGGAAGCTACACTGCAGTT CCCAATACTACTTCAGCATAGGCA AAAATGTGAAGCCAATTAAACAGAGA AATCATTGGCATTATTGGCAA TCAAAGCTT	Slightly induced in Individual 3, but not Individual 4 or Individual 5	NM_001007
88	G + AP1	clone RP1-88D18 on chromosome 11p12-13	231bp		Very high expression in Individual 4 and Individual 5, but not in Individual 3	AL133330
89	G + AP36	Human mitochondrial DNA	28bp	GGGGGGGGGGATATGGGTGCGA AGCTT	Induced in Individual 5, but not in Individual 3 or Individual 4	NC_001807
90						

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
91	C + AP39	ecto-ATP diphasphohydrolase	113bp	AAGCTTCCAGCTACACCTTC CTTTGTACTTGTGCTGTATAGGT TTAAAGACCTGACACCTTCATAA TCTTGCCTATAAAAGAACATTATT GACTTTGTCTAG	Induced in Individual 3, but not in Individual 4 or Individual 5	AJ133133
92	C + AP3	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 9kD (ATPSH)	131bp	AAGCTTGGTCAGTAGGGAGAGCAC GTTCAAGGGAAAGGCCATCTCAA CAGAATCGACCAAACCTATACTTTC AGGATGAATTCTCTCTGCCAT CTTTGGAAATAATTTCTCCTCTT TCTATGG	Induced in Individual 3, but not in Individual 4 or Individual 5	NM_003945
93	A + AP3	cyclin D2	265bp	AGGTCAAGGTGAGTTATTGTCCAA ATAGCATAACCTAATTGCAATTCAA ACCATTTCAAATCCATCTTTAAAC TAGTCAGAAAAACAGGGTTATTATT TTAAATCACTTAACACTGAACAGA TAAGACCTCTAAAAGGCAGCTGA CTATATCATGTCACCATAGCICA ATACAACATTGGCCATACCTTCCT AAAAACCTTCGCAATACACTGATC ATGCTACTTATCAGCACCTTCAAC ATCCTGACCAAAGCTT	Induced in Individual 4, but not Individual 3 or Individual 5	NM_001759
94		no insert - just vector				
95		No significant match to anything	122bp	AAGCTTCGACGGACACCAA GAACAGAGAAAGTAAAAGATTAAAGT GTTCTGACATTTCCTACAATGATCT TGGCTTCTGACCAATTGTTTCT CCTACCAAGTACTTGCTCAGTGT	Induced in Individual 1, but not in Individual 6 or Individual 7	
96						

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
97	A + AP8	Inhibitor of apoptosis protein-1 (MIHC)	310bp	<pre> ACCAAGN GTTTGC AAGC ATGGTT CCTGGATCTNACAGACGTTGGGCT TTTC AACTGCAGACTTCATGCTT GTTTCCAGGTGGAGGANAACAT CACATCTCATTACCAACAATTATT CCCTCAAGGTAAGTAATTGTATCT AACTTCAAA TATTCCCTTCCCTGGCC AAAAAATTTCACATTTGTTAAAAAA TCTTCTTTGATTCACTCACTGTCTT ATTTAAATTCTTAAGTTCTTCATT TCCTAAAATGTAACCTTCAACACC ATTCTCATCCTCATCATTCAGCG GTAAAAGCTT </pre>	Induced in Individual 7, but not Individual 6	AF070674
98	A + AP8	ribosomal protein L35a (RPL35A)	441bp	<pre> ACAAGAGCACA AAATCC CACATT ATT TATTGATT TTTCGTTAGTTAAATCC TTGAGGGTACAGC ATCACTCGGA TTCTGTCCAATGGCCTTAGCAG GAAGATGCTTCGGAATTTGGCAC GAACCATGCCACTGTTTCCATGGG CCCGAGTTACTTTCCCAGATGA CTCTGGTTTGTTGGTTGGCGCC AGGAGTGA CTGTGTTCTCTTGCT TTATATACAATAAGGCCATCTCTGC CCAAATAGAAATTCTGTTTCATCTCG GGGTAAACACCTCAATTTAAAGA AGAGCTGTGCTCCCTGGTT CGGAGAACCCCGCTTATAGCCAGCA AAAATGGCCTTGGACCCACAGCCTT CCAGAGCATAGTTCCCTTTAGAAAGT CCGTTCCAGCAGGCTCCACAG GAGCCAAGATGGGGTAAAGCTT </pre>	Induced in Individual 7 and not in Individual 6	NM_000996

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
99	G + AP10	ribosomal protein S12	443bp	AAGCTTCCACGTAACCCCACGCCA TGCCCGAGGAAGGCATTGGCTGCTG GAGGTGTAATGGACGTTAACTCTG CCTTACAGGAGGTTCTGAAGACTG CCCTCATCACGATGCCCTAGCAC GTGGAATTGCGAAGCTGCCAAAG CCTTAGACAAAGGCCAAAGCCCCATC TTGTGTGCTTGCATCACAACGTGTA TGAGCCTATGTATGTCAGTTGGT GGAGGCCCTTGTGCTGAAACACCA AATCAACCTAAATTAAAGTTGATGAC AACAAAGAAACTAGGAGAAATGGGTA GCCCTTTGAAAAATTGACAGAGAG GGGAAACCCCGTAAGTGGTTGGT TGCAAGTTGTAGTAATTAAAGGACT ATGGCAAGGAGTCTCACGCCAAAGG ATGTCATTGAAAGAGTATTCAAATG CAAGAAATGAAAGAAATAAATCTTG GCTCAC	Very high expression in Individual 1 and Individual 7, but not Individual 6	NM_001016
100	G + AP10	Thymidylate synthetase	196bp	GCAGAACACCTCTTATTATGCAA CATATAAAACAACTATAAGTTCA AACCACACTCTACATCATGATCGAT GGTGTACTCAGCTCCCTCAGATT NGAGGGAAATAGCTNGTGAATTCT TAAAATATTCTAAAATATTCCAAA ATAGCTNGTGAATNCACCAACCTT CTTTATAAGTACGTGGAAAGCTT	High expression in Individual 6, but not in Individual 1 and Individual 7	NM_001071

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
101	G + AP12	chromosome 17, clone hC1T.211_P_7	314bp	GGAAAGTAGGTATTTCAATTTCATTTTAAAGCAGGTGCTCCCAAACCTTTCAC AGCGTACACCTNGAGGGTGGAGAA CATCCAACCNACACTGGATGGTGG ATGGGACCCACTCTGGTAACCT GATGAGGAAGCTCTAGGTGTANAAA TTCAGGACGGGTCTTCAAGTCCCTGTT AGGGCTTGGTTCAAGTCCCTGTT TGCCACTTACTAACTGCATGACCTT GAGCAAGCCACTTAATTCTCTGCT CCCTCTCTGTGAAATGGGTACAATG TGTCAGCAGTAAAGGAACTAATAA CACGTACAGCACTCAAGCTT	Higher expression in Individual 1 and Individual 7 than in Individual 6	AC003665
102	G + AP19					
103	G + AP19	just vector				
104	A + AP3	cyclin D2	265bp	AAGCTTTGGTCAGGATGTAAAAAG TGCTGATAAGTAGCATGATCAGTGT ATGCCAAAAAGGTTTTAGGAAGTAT GGCAAAAATGGTTATGGCTATGA TGTTGACATGATATAAGTCAGCTGC CTTTAAGAGGTCTTATCTGTTAG TGTTAACGTGATTAAAAAAATAATAA CCTGTTTCTGACTAGTTAAAGAT GGATTGAAATGGTTGAATGCA ATTAGGTTATGCTATTGGACAATA AACTCACCTGACCT	Induced in Individual 1, but not in Individual 6	NM_001759
105						
106		just vector				
107		just vector				

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
108	C + AP16	clone DKFZp584Q092	355bp	AAGCTTAGAGCGTCAGTAAGCGA GAGAAAGGACGGGAAAACGAGCA AATGTCAATGAGCTCACAACTTCATT CCCTTACACACTTCAGTGACATCAG TGCTTGTACAGGGGGAACTGTTCA TCTTGATGAGGATCAGAATCCTATT AAGAACGGGAAGAAGATAACCTCAG AAAGGTGCGAAGAAAAAGGGTTT CGGAGGGGGGGTGAATTATGGGT GTACATATTGTATAATTGTCTCAT CCTGAGATACTCTAAATTCTATTGT ATATAGGTGGTTTCCCTGGAAATC ATTAATTGTTGCTTGGACATGTG GAAAGAGCCTTACTAATAAAATTGA TTTACTTATG	Strongly induced in Individual 1 and not in Individual 6	AL050003
109	C + AP9	cDNA FLJ11508 1s, clone HEMBA1002162	150bp	CCATCAAATGTAATTATTTAAATAA CAATTCAATTGCATGTTAAGTAAAC CAGTTGTAGCAATAAAAAATACAG AATTGGAGAAAATCTGGCAAATTAA AACCTGTATCTAAATGCAGGCAATT CTGTGATACTACGGAAATGAAGCTT	Slightly induced in Individual 1 and not Individual 6	AK021570
110	A + AP22	mitochondrial genomic DNA	64bp	AAGCTTTGATCCAAGCCTACGTTT TCACACTCTTAGTAAGCCTCTACCT GCACGACAAACACAT	High expression in Individual 6, but not in Individual 1 or Individual 7	NC_001807
111	A + AP20	NADH dehydrogenase-ubiquinone Fe-S protein 2 precursor	69bp	AAGCTGGTGTGCATGTTACTAAAAA AGGAGAAAATTATAATAATTAGCG TCCTGGGCCCTAGGCCT	High expression in Individual 6, but not in Individual 1 or Individual 7	AF013160

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
112	C + AP9	No significant match to anything	165bp	AAGCTTCATTCGGAGGGTACCGTT TTAGGCTCTTATTGACCATTCTGAA CAGCGTGCTGTCTTCTTTCTTGGTT AAGTTTCTCTGGCTAACCTCTTTAA TGTTTCCCTTTAAATGAAAACCTGG CTTCGTTCCAACCTCCCTCTGG GCATGGCTCTTTGG	Induced in Individual 1, but not in Individual 6 or Individual 7	
113	C + AP9	cytochrome b gene	233bp	AAGCTTCATTCGGATAAAATCACCT TCCACCCCTTAACCTACACAATCAAAGA CGCCCTGGCTTACTTACCTCTCTCCT CTCTCCCTTAATGACATTAACACTAT TCTCACCAAGACCTCTAGGGGACC CAGACAATTATAACCCCTAGGCCAAC CCTTAAACACCCCTCCCCACATCA AGCCCAGAATGATAATTCCCTATTGCG CTACACAATTCTCGATCCGTCCT AACAAACTAGG	Induced in Individual 1, but not in Individual 6	AF254896
114	C + AP11	just vector				
115	C + AP10	lysosomal pepstatin insensitive protease (CLN2)	157bp	AAGCTTCACGTAGTATTGAAATGG CCAGTTTACTTGTCTGCCTTCCTT CCAAGACCGTGGCTCTAGAGGA CTAGAATGTTGCTCTATTAACTTT GTGTTCCAGGTCCTAGCTCAGGA GTTGGCAAATAAGAATTAAATGTCT GCTACACCG	Expression in Individual 6, but not in Individual 1 or Individual 7	AF039704
116	C + AP19	clone 108K11 on chromosome 6p21	52bp	CAACAAAAATTCTTACCTCATTT TCGTTCTCATGTTAGGCATAAGC TT	Induced in Individual 7, but not in Individual 6	285986
117	C + AP19	No significant match to anything	117bp	AAGCTTATCGCTCACACTGTCAATGT TGAAATTAAACCTGTGGCTTTGTA ACAAGAAGGAATGAAATTATACTGA AGTAAAAGTCTGCAGTTATGCCCA AATGAGATGACCCCTGG	Induced in Individual 1, but not in Individual 6	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
118	C + AP19	No significant match to anything	213bp	CTAGGTCTCTTCCAGTCCTCTAC CTCTCTAAACTGAATCTCTCAAAA GCCTCCTGTCTATCCTGAGTGGTT ACTGGGCTGACCTCCAAACTTTCCA ATGAAACGGGAGGTGAAAATGGTAA ACTGGAGGTAAATGAGGAAGGGTCA CAACTGGATTTCACAACTAGGGATCAG AGAAATCAAAATCTTGAGGAGCTTC AACTTGCTTATATCTT AAGCTTGGCATGGAAAGAATGAAT AGCAAAAAAGGAGAAATTTTTAA AAAGATCTCTCACTGGG	Repressed in Individual 6, but induced in Suzanna	
119	C + AP23	No significant match to anything	66bp	CAACATCACCAAATAATTATGG ACTCAGAAATTAAAAGAACATTGAC AGTTATGAATGCAATGTTATTCTG AAACTCTAATCTAGTTGACAACTA ATCCGTGACAAATTACAGATTAAAT TTTACTTTATTTCTTCAGGCCTGGG GTTTTTCGATGACTTCAAATTGGG ATCTTCQAATTGAAAGTGGAAAT GTTTCATGTCGCAATTACCAAAACAA TTTGCTTGGCTGAGCTAAAAGCTCCCT CTCCAGCTCTTGCTGATACTCTGAA CTAGCATCACAGGGTCTCCAGAT GTCTGTGCGTTAGATTGTATTCTC TAATCTTGTCACAAAGAGTTCTG TATAGGATCAAAAGCTT	High expression in Individual 6, but not in Individual 1 or Individual 7	
120	C + AP22	mitochondrial ATPase coupling factor 6 subunit (ATP5A)	366bp		Induced in Individual 7, but not Individual 6	M37104

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
121	C + AP19	clone 717M23 on chromosome 20	363bp	CCAATTTCTCAATTATTGAGTTA CCACCAAAAGGTAAATTAAACAAT GTGATAGAGGGTGCAGTGACGTT CATTAGTACAAACATGGCTATGTT TATAAAATTATAGCTGATCAACTA GAGAATAAATAATTATCCCTTTAT TTAGGTCTCTTTACATTGACGTT CTTCACAGGGAAATTGACAAAACCC TTCACACAGGAATTGACAAAATCAA GGAATTGAGGAAGGCTCTTACTGCG TGGTATCCATTGGCAGCTTGTC CAGAAGTAGGGACAGCTGCTCCT ATCCAAGAACACGTCCTCATCAC TGTTGAGGGAAATCCCCACTCTGGT CGAGCGATAAGCTT	Gene expressed at same level in everyone	AL050321
122	C + AP19	clone RG013F03	126bp	CGAAAATAGAAAAATGTATTACAA GTAGTACGTTACTATGATGAGAAAG CACAAAGACACCCGTGCTATAATA CATGCCATTGGCTCGAGAAGAAACT ACGGAACACCCCTGCAGCGATAAG CTT	Repressed in Individual 1, but not in Individual 6	AC005046
123		just vector		GCAGAACACCTCTTTATTAGCAA CATATAAACAACTATAAGTTCAT AACCACACTCTACATCATGATCGAT GGTGTACTCAGCTCCCTCAGATT GAGGGAAATAGCTTGTGAAATTCTTA AAATATTCTAAAAATATTCCAAAAT ACCTTGTGAAATTCAACCAACCTCT TTATAAGTACGTGGAAGCT	High expression in Individual 8 and Individual 4, but not Individual 9	NM_001071
124	G + AP10	thymidylate synthetase	196bp			

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
125	G + AP19	clone RG013F03	126bp	AAGCTTATCGCTCGAGGCCAATGCA CGTAGTTCTCTCGAGCAGGTGCTTG TGTATTATGCAGCAGGTGCTTG TGCTTTCTCATCATAGTAACGTACT ACTTGTAAATACATTTCTATTTTC C	High induction in Individual 4, but not in Individual 9	AC005046
126	G + AP19	clone RG013F03	126bp	GGAAAAATGAAAAATGTATTACAA GTAGTACGTTACTATGATGAGAAAG CACAAAGACACCTGCTGCTATAATA CATGCATTGGCTCGAGAAAGAGACT ACGGAACACCCCTGCGAGCGATAAG CTT	High induction in Individual 4, but not in Individual 9	AC005046
127		just vector		CAGGAGGCATGCAGGGAGGACAC TGCAGATGATCAAAGTTTATTAAC CATTATAGAACACTAAAAAATAAAC AATATGATTGCATTTCGTGGTGA ACTTTGAAAAATGTTTCAAGCACA CATAAAAAGCAACAAAGTTTACCCC ACAAGGTATGCTATGCAGCCAGTC CCTAACTGCTGGGTCAGCACGTGC TCTCAACAGACAGCTGGGTAGGA GTAGGGCTGCTGGTCCCTGAG GCAGGGCTTCCCTACTCGGAA TGAAGCTT	Repressed in Individual 8 and Individual 4, but not Individual 9	AF147336
128	C + AP9	clone YB26B05	276bp			

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
128	C + AP9	uncoupling protein-2 (UCP2)	267bp	AAGCTTCATTCCGCTCCTTACCTA CCACCTCCCTCCCTCCACCTCT TCCTTCCGGTCCCTAACCTACCC TCCCCTCTTCTACATTCTCATCTA CTCATGGTCACTAGTGCTGGTGGAG TTGACATTTGACAGTGTTGGAGGC CTCGTACCAAGCCAGGATCCCAAGC GTCCCCGTCCCTGGAAAGTTCAAGC CAGAAATCTTCTGTCCTGCCCGAC AGCCCAGCCTAGCCCCACTTGTCA CCATAAAGGCAAGCTAACCTTGG	Repressed in Individual 8 and Individual 4, but not Individual 9	AF096289
129	C + AP16	Cide-b (CIndividual 3)	385bp	AAGCTTAAAGGCTGAAAGCTTGGCA GTCACCTGAGTAAGTCACCTGGGT TCAGAGCTGAGGGTACTCCATGG TGACAGCTGAGGGTTCCCTCTGG AACTTCTGGCTGGTGGTCTCT CCTGTGCTGGGGCTTTAGTGGTGT TTCTCTGTTACAACCTGGGATGCTCA GCCCAAGGACAAGGTGGGAATGAGT CAAGGCCTGGACTCTGGCCCCCTG CCTGGCCAGTAAGAAGGGCAAAGT CCAAGGGGGATGAGGGAGGG GCCAGAGATGGGGTCCTGGAGGAAG AATTGGCCTGGCAAAAGCCATTGGA GCTTGTATGTTGCTTTGGTAGATGG ACATGTGTTGAGGGTAGATGGG ACCATGTAAAAGGATGAAATGTG	Induced in Individual 9, but no in Individual 8 or Individual 4	AF218586

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
129	C + AP16	No significant match to anything	385bp	CTGGAAATAAAACTACATCTCAAAA CCTCTTGCACCAACCAGGTGAGTA TGTTTCACCAATAAGACATAAGCA GATAGAGGATGCAAAGTCACCTCC ACAAAACATCTTATAAGCCAGCTG ACACATACCCATTCCACCATATCAT GTTATGTAGTCTCAGGGTTGCTGC AGAGTAATTGTCCTCTTTAGACATG GTAGAGAAATTATGTACAGTGGAG CAGAGACTGCAGCAACTACAGACT TCAGCCACATAACTTACTCTCTAT TATAAGACAGCAAGAAAACAGACTT ATCTTCCAGAGTCAACAGCTGGT ATCCAGAGAAGGGAGAAAGGGATAAC AAGTATGTGCACTCTGAATATGAAC ACTACGCTCTAAAGCTT	Induced in Individual 9, but not in Individual 8 or Individual 4	
130	G + AP43	mitochondrial DNA for D-loop	230bp	GGGTATGCAACGGGATAAGCATGG AGACGCTGGAGCGGGAGCACCC ATGTCGCAGTATCTGCTCTTGATT CTGCCCTCACTCTTATTATTTATCGCA CCTACGTTCAATTACAGGGCGAAC ATACTTACTAAAGTGTGTTAATTAT TAATGCTTGTAGGACATAATAAA CAATTGAATGTCAGCAGCCGCT TTCACACAGACATCATAAACAAA ATTCCAC	Induced in Individual 1, but not in Individual 6	AJ230610

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
130	G + AP43	no significant match to anything	260bp	GAAATTGGATTAATTCTTTATTC ATTCTTGCAACTTTCCATGCTTT GAAATTATTAGAAGTTAACAAA TAAGCAAACAAACTACAAATCAGGA ATGGAAAAGTGAATTACAAAATGC CATTTTCAGATTACAAGACGCTTG CATTCACCTTCCTTGACGATTACT ACTTCTTACACCGCTATGATTCTCT CCTTTTCCACCCACACGGCTCCA GGTCTACTTGTCTTTACTCTCCCCG CTTCAAGCTT	Induced in Individual 1, but not in Individual 6	
131						
132						
133		No insert - just vector				
134	G + AP47	chromosome 10 clone RP11-70E21	257bp	GAGATAGAGTCCTGCTGTACCT AGGCTGGAGTGCAGTGCATGATGTC ATAGCTCACTGCAGGCTCAAACCTC TTAGGTTCAAGTAGATTCTCCACCT CAGGCCCTCTGAGTAGCTGAGATTA TAATTTTTTTTTGTAAGATGGGG TCTTGCTATGTTGCCCAAGGCTGG CTCAACCTCCCTGGCTCAAGTAAT CCTCTGCCTGGCTTCTGGAAATT ACGGGCATAAGCTT	Induced in Individual 1, but not in Individual 6	AC016399
135	A + AP41	matches a bunch of sequences that make no sense	158bp		Induced in Individual 1, but not in Individual 6	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
136		Jun B proto-oncogene (JUNB)	112bp	ACTAAATAGATTCAATAAAAAGAA CAAACACACACACAACAAACAAACACG TCTTAAAATAAACTCTTTANAGACT AAGTGCCTGTCTTCACAGTA CGGTGCAAAAGCTT	Induced in Individual 1, but not in Individual 6 or Individual 7	NM_002229
137		Chromosome X clone bWXD501	63bp	AATAAGAACAAAAAGAAATTATT ACAAAATTCTTACTTGACCACTAGT GTCAGGCCAAGCTT	Induced in Individual 1, but not in Individual 6	AC004677
138		No insert - just vector				
139	A + AP47	Chromosome 16 BAC clone CIT987SK-A-67A1	106bp	AGATATAGAAGTCCCACTAGGTTG CCCTGGCTGGCTTAACCTCTGG TTTCAAGTGATCCTCTGCCTGG CCTTCCAATAATGCTGTATTACGG GCATAAGCTT	Induced in Individual 7, but not in Individual 6.	AC004531
140	A + AP47	Chromosome 16 BAC clone CIT987SK-A-67A1	106bp	AAGCTTATGCCGTATAACCAGCAT TTGGAAAGGCCAAGGCAGGAG CACTGAAACCAAGAGTTAACGACC AGCCAGGGCAACCTAGTGGACTT CTATATCT	Induced in Individual 7, but not in Individual 6	AC004531

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
141	C + AP41	No significant match to anything	464bp	CAGGGGGGGGACCACTCAA ACTATTTAAACCTTACAGCAACGT GACCGTGATAATTACAAATTAT AAGTGGCTGAGGATTCTTAAATAAA ATATAAGGATTGAAATTAAATATT CAAACATCAAGAAAATGACACATA TGTAACAATAATCCAGACTAAAGAA ATGTAGGCATTGGTCATAATTATTA CATTTTAACCTTTAAAAAAATGA GATATTATAGATAAAAACAACTCTCC ATCTCATTCCTCCTACCTCTCTCC AAATATAGTCACTATTCCCTGAAGTA TGTTTGCATTCAATAGCAATTTTATTA TTTAGTATTGCATACTTGATGATG CAAGTAAAACTAACCTTAACTTAACT GCTACATCAGAGACTTTAGAATTGA AATTGACITCTCTGAGCCCTCAGAAT CTTCATAATATTCTGGCCTAGCC ACCCCGTAAGCTT	Induced in Individual 1 and Individual 7, but not in Individual 6	
142	C + AP41	Fc-gamma-receptor IA (FCGR2A)	240bp	AAGCTTACGGGTCACTACATA CAAGCATAAGCAGACTTAACTTG GATCATTTCTGTTAAATGCTTATGT TAGAAAATAAGACAACCCCAGCCAA TCACAGCAGCCTACTAACATAAA TTAGGTGACTAGGGACTTTCTAAGA AGATACCTTACCCCCAAAAACAAATT ATGTAATTGAAAACCAACCGATTGC CTTATTTGCTTCCACATTTC ATAAAATAACTTGCCTGTG	Induced by penicillin in Individual 1, but not in Individual 6	M90727
143	C + AP45	Chromosome X clone bWXD501	67bp	CGATAATAAGAACCAAAAGAAATT ATTACAAAATTCTTACTTGACCAG TAGTGTCAAGCCAAAGCTT	Induced in Individual 7, but not in Individual 6	AC004677

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
143	C + AP45	clone CTA-407F11 on chromosome 22q12	64bp	AAGCTTGGCTGACAAATCTCAGAGG TCACCTTTATAGAAAAATATAGTCT AGGCTTAGGTTCCCTG CAAACAGTATAATTATTTACAAT AGCAACCAACTCCCCAGTTGTTTC AATTGTGACATCTAGATGGCTTAAG ATTACTTCTGGTGGTCACCGCAA GCTT	Induced in Individual 7, but not in Individual 6	AL022329
144	C + AP48	3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene	104bp		Repressed in Individual 1, but not in Individual 6	U80460
145	G + AP53	SH3-containing protein EEN (EEN)	253bp	GTAGAAAGAGACATTTAATACTTCT GTTTACAAAATTCAAGGCCGTACATT CAGTTGCCCTGNACCGTGCCCCA AGCTGTGTGCTCATCTCTGCC CTCATGTACTTCTGACGGGGGG TGCAAGGGCAGGGCAGAGCAGAGC CTGGGGTCCGGAGGGCTTCACTGGA CCACAGGGGAGGGGAATGTGAAT GTGGCTGTGCCAGAGAACCTCCCA TTTCATCGATTTGCAATTGGCGAT AGAGGAAGCTT	Induced in Individual 6, but not in Individual 1 or Individual 7	AF190465
146	G + AP53	SH3-containing protein EEN (EEN)	255bp	GTAGAAAGAGACATTTAATACTTCT GTTTACAAAATTCAAGGCCGTACATT TCAGTTGCCCTGACCGTGCCCCA AAGCTGTGTGCTCATCTCTGCC CCTCATGTACTTCTGACGGGGGG GTGCAGGGCAGGGCAGAGCAGAG CCTGGGGTCCGGAGGGCTTCACTG GACCACAGGGGAGGGGAATGTG AATGTGGCTGGGCCAGAGAACTC CCCATTTCATCGATTTGCAATTGGG CGATAGAGGAAGCTT	Induced in Individual 6, but not in Individual 1 or Individual 7	AF190465
147						
148						

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
149	G + AP55	No significant match to anything	287bp	GTAATTGGTTGAGTTCAATTGTAG ATTCTGGATATTAGCCCTTGTAG ATGAGTAGGTTGTGAAATTTC CCATTTGTTAGGGTGCCTGTTCACT CTGATGGTAGTTCTTGTGCTGTC AGAAGATCCTTAGTTAATTAGATC TCATTGGTCAATTGGTCTTTATTG CGTTGCCTTGGTGTGTTGGACAT GAAGTCCGCCATGCCTATGGC CTGAATGTTAATGCTTAGTTTCT TCTAGGGTTTATGGTTTATGTC TAACGTAAGCTT	Induced in Individual 1, but not in Individual 6	
150	G + AP54	ribosomal DNA complete repeating unit	215bp	AAGCTTTGAGGTCAAGGAGTTCGA GACCAGCGTGCCCAACGTGGAGA AACCCGCTCTACTGAAATAGG AATATGAGCCGGCGTCATGGTGT GGCCTGTAATCCAGCTACCGAA GAAGAAATCACTGGAAACCCGGAAAG CAGAGGTTTCAGTGAGCCGAGAGA GCGCACCGCACCGCAGCCTGGG TGACAGAGCGAGAGAGACTCAGTC C	Induced in Individual 1, but not in Individual 6	U133369
151	A + AP52	heat shock 60kD protein 1 (chaperonin) (HSPD1)	241bp	AAGCTTGACCTTTATAATGAACTG TGACAGGAAGGCCAAGGCAGTGT CCTCACCAATAACTTCAGAGAAGTC AGTTGGAGAAAATGAAAGAAAAAG CTGGCTGAAAATCACTATAACCATC AGTTACTGGTTTCAAGTTGACAAAT ATATAATGGTTTACTGCTGTCATTG TCCATGCCTACAGATAATTATTT GTGTTTTGAATAAAAACATTGTT ACATTCCCTGATACTGGGT	Induced in Individual 6, but not in Individual 1 or Individual 7	NM_002156

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
152	A + AP52	cDNA FLJ20436 firs, clone KAT03972	204bp	AGGGAGGTGCTAGTAGTACAGAGGA ATCCCTTTATGATCAACTAGAGTCT GGGTCCCTCACTTCAGTCGAGTG CTGTCCTCATTAGACCACAGTAAG AGTTAACAGGTACCAAATGGCAGT CGCATCTTCTGGGTAAAGGCAGTG TCTGGTCATTGGAAAGAGACTGATT GGAACAACGAAACATCATCCACAAA GGTCAAGCTT	Induced in Individual 6, but not in Individual 1 or Individual 7	AK000443
153	C + AP55	No significant match to anything	407bp	AAGCTTACGTTAGAACCTGCAATAT TCTCGTGTGTTGTTGCTCTCTT CCTGTCAACAGTGTGTTATGCTTCC CAGCAGCAGACACGTATGTTGTA CACACATACTCATTCAATTATTCAATT TTAGGAGAAGGCCATTACACATGA AAACAAATTGAGATTAAATGGTAGTG TTTTAGGACCAGTGGCTGGGGC TAAAGCAATTAGGAATTAAACCATT CCCCTTCTTAATAGGATAACGCCCT TGAGGAGAAGTGTGGTCATATTCT ACAGCCTCATATAATGTTAAAGTCAGT GTCTTCATCACATGGACTCAGCATA CTCTTAGAAGCTCCTTTAGTGGGT CAAATCTAGATNTACTTGGCCCAT TTTATTATTG	Repressed in Individual 1 and Individual 7, but not in Individual 6	
154	A + AP47	Sid3177 mRNA (this is a mouse gene)	95bp	AAGCTTATGCCGGGCTGAAAAAC TCAATTATGTTCATGACAGTGGGG ATTTTTTAAATGTCTACATTCTTC TAATAAACTGTTGAAAGACT	Induced in Individual 8 and Individual 10, but not in Individual 9	AB024935

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
155	A + AP47	Chromosome 16 BAC clone C17987SK-A-67A1	106bp	AAGCCTATGCCCGTAATACCGCAT TTGGAAAGGCCAAGGCGAGGAGAT CACTTGAACCAAGAGTTAACGCC AGCCAGGGCAACCTAGTGGACTT CTATATCT	Induced in Individual 10, but not in Individual 9	AC004531
156						
157	G + AP41	ribosomal protein L8	218bp	GGCATAAACACAACTTATTGAGG CCCTCAGGACTAGTTCTCTTC TGTCAGTCTGGTCCCCGGAGA CGTCCAGTCCGGCGGGCAGCAA GAGACCCCACCTTGGGCCAGGAGG GCACATCTCTGGGATGTGCTGGTGGTGC CCTGGCGATGTGCTGGTGGTGC CACCTCCAAGGATGCTCCACAG GATTCAATGCCACACCCGTAAGC TT	Induced in Individual 10, but not in Individual 9	NM_000973
158	G + AP41	tapasin (NGS-17)	58bp	GGAAAGCACTGGAATAACAGCTTTATT CCTACACGATTAGACCCGTTACCC CGTAAGCTT	Induced in Individual 10, but not in Individual 9	AF029750
159	G + AP47	CoREST protein (COREST protein)	149bp	AAGCTTATGCCGGAAACAAAAAC GGGAGGGGGAGGGAGGGGAGGAT GAACCTGGAAAGGGCAAATGGAAAC AATCCCATTGACATTGAGGGTTGATC AAAACAAGGAAAGCAAAAAGGGAGG TTCCCCCTACTGAGACAGTTCCCT AGGTC	Induced in Individual 10, but not in Individual 9	AF155595
160	G + AP43	mitochondrial DNA hypervariable II region	104bp	GTAAGCACATAATAACAATTGAA TGTCTGCACAGCCGCTTCCACAC AGACATCATACAAAAAATTCCAC CAAACCCCCCCCCTCCCCGCTTC AAGCTT	Induced in Individual 10, but not in Individual 9	AF278478

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
161	G + AP52	clone RP11-517O1 on chromosome X / FLJ23025 fs, clone LNG01702	71bp	GGAGACAAAATACAGTGGCATTAC TGGAAAGGAATATCACAAACATTACAT TTTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
165	G + AP52	clone RP11-517O1 on chromosome X / FLJ23025 fs, clone LNG01702	71bp	GGAGACAAAATACAGTGGCATTAC TGGAAAGGAATATCACAAACATTACAT TTTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
167	G + AP52	clone RP11-517O1 on chromosome X / FLJ23025 fs, clone LNG01702	71bp	GGAGACAAAATACAGTGGCATTAC TGGAAAGGAATATCACAAACATTACAT TTTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
163	G + AP52	clone RP11-517O1 on chromosome X / FLJ23025 fs, clone LNG01702	71bp	GGAGACAAAATACAGTGGCATTAC TGGAAAGGAATATCACAAACATTACAT TTTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
169	C + AP48	No significant match to anything	103bp	CAAATTGTATTCTTTAATGAAATT AATATTCTCAACTAGTATCAATGCT TTGTCAATTATAAGTGTGACTTCA ATATTTCCCTCCCTACCGCAAG CTT	Repressed in Individual 8, but not in Individual 9	
164	C + AP45	dynamitin (dynactin complex 50 kD subunit) (DCTN-50)	61bp	CAGAGTACAACAGCATTAATGGTC AGAAAACAGTTGTACAGTATTACAGT CAGCCAAGCTT	Induced in Individual 10, but not in Individual 9	NM_006400

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
166	A + AP3	cyclin D2 (CCND2)	265bp	AGGTCAAGGTGAGTTTATTGTCCAA ATAGCATTAACCTAATTGCATTCAAA ACCATTTCAAATCCATCCTTAAAC TAGTCAGAAAAACAGGTTATTATT TTTAAATCACCTTAACACTGAACAGA CTATATCATGTCCACCATCATGCCA ATACAACATTTCGCATACACTTCT AAAACCTTTGCATACACTGATC ATGCTACTTATCAACACATTCTAAC ATCCTGACCAAAGCTT	Induced in Individual 11, but not in Individual 12	NM_001759
167	C + AP24	chromosome 16 clone RP11-296I10	246bp	CCATACATAGGCTTGAACAGGGTT CAGCCAACCTCTCTGCAGAGGC CAGAAAAGTAACAGTTCTCAGGGAA CTGTAGTCACTGTTGAGTTACTCA ACTTTGCCATCCTAGTGTGAAAAGC AGCCACTGGCAATACATAAAATAAT GGTGTGGCTGTTCAATAAAATT ATGTATAAAAACAGGTAGTAGACTG GATTTGCCCTAAGTGTGTAGTTT TTGATCTATGGCTAGTGAAGCTT	Induced in Individual 5, but not in Individual 12	AC009060
168	C + AP24	No significant match to anything	253bp	CGAGATTAAATCAGAAAATTGTATC TACAATAATTGACACAATCTCACTTC TTGTCCTCACCCATCTCATCAAAA ATTATTGCATTTCCCCTGTGAATAT ACTCATTTGGATTCCTCTGTGAATAT GCATCTGGTTAAATCCATCTTA AAAAAGGAGAAGGGTACATATG TGAGGGCAAAATATTCTCTTGAAGC CAACAGATAACAGAGTTGCTAGTGA AGCTT	Repressed in Individual 11, but not in Individual 12	

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
168	C + AP24	NADH dehydrogenase	254bp	CATTTTATTATTAGGACTACAT AACACATTGCATGCTACATAATACA CTGTAAACCTCTAGCAGGGTAGA TGGCCATAACTGAGTTATTITTC ATCAATCAGGAAAATGCTTCCCTAA TCAATGTTCTCCAACCCCTTGTACA CATAGTAACGATCAACTCCAGAGAT GCGCCTATCTCTTCATCAGACTC CAGTGATAACCCAAAATGAGCAACC CTTTTTCTTGGCCCCGGCTAGTGA AGCTT	Repressed in Individual 11, but not in Individual 12	X81900
169	G + AP5	alpha-L-fucosidase	153bp	AGCTTAGTAGGGCTATGGCA ACTCTCCAGAAATTTCAGAGCAAT CTAAAAAGGCCAAAATTGCTATGT TTACAGTGATACTATTAAAGAAAATG ATATGTGATTCTGCTGTCTTTTA AGTATGATCAAATAAAAATTGTA CATC	Repressed in Individual 5, but not in Individual 12	M29877
169	G + AP5	latexin mRNA	139bp	AAGCTTAGTAGGGCCAAATAATCCCA AAGTGTCACTTATAAATGTCTT GATTACAGTATAAGAACCTTATAGAG TCCATAATACAAAGTATCACTACAT AAAAATGTCCTTAAACAGTAATAG TGGTATGTATATCC	Repressed in Individual 5, but not in Individual 12	AF282626

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
170	G + AP10	manganese superoxide dismutase (MnSOD/SOD2)	294bp	AAGCTTCCACGTATAAACATAAAATT GTATTTCCTGTTTAATTCCAGGGG AAGTACTGTTGGAAAGCTATTAT TAGGTTAAATGTTTACAAATTACTG TTTCTCACCTTCAGTOATAACCTAA TGATCCCCAGCAAGATAATGTCCTGT CTTCTAAGATGTGCATCAAGCCTG GTACATACTGAAAACCCCTAAAGGT CCTGGATAATTTCGTTGATTATT CATTGAAGAACATTATTTCCAA TTGGTGAAGTTTGACTGTTAAT AAAAGAATCTGTCAACCACATC	Repressed in Individual 11 and Individual 5, but not in Individual 12	X65965
171	G + AP10	metallothionein-1G (MT1G)	137bp	GGGAATCAAGTCTAAGTGTAAATT ATTATTCAACATATTTCACAGAAAAA AAGGAATGTAGCAAAGGGTCAG ATTGTAGCAAAAAACAAAAATCT GGATTTACGGGTCACTCTATTAT ACGTGGAAAGCTT	Induced in Individual 11, but not in Individual 12	J03910
172	A + AP23	cyclin D2 (CCND2)	179bp	AGGTCAAGGTGAGTTTATTGTCCAA ATAGCATAACCTAATTGCATTCAA ACCATTTCAATCCATCTTTAAC TAGTCAGAAAAACAGGTTTATTATT TTTAAATCACTTAACACTGAACAGA TAAGACCTCTAAAGGCAGGCTGA CTATATCATGTGACCATCATAGCCA AGCTT	Induced in Individual 11, but not in Individual 12	NM_001759

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
173	A + AP3	cyclin D2	265bp	AGGTCAAGGTGAGTTATTGTCCAA ATAGGCATAACCTTAATTGCATTCAA ACCATTTCAAATCCATCTTTAAAC TAGTCAGAAAACAGGTTATTATT TTAAATCACCTAACACTGAACAGA TAAGACCTCTAAAAGGCAGCTGA CTATCATGTCAACCATAGCCA ATACAACATTTGGCCTAACACTTCT AAAAACCTTTGCATACACTGATC ATGCTACTTATCAGCACTTCTAAC ATCCTGACCAAAGCTT ACATTCTTCAAAAGGGTTCTTATA GAECTGTCCATGCTCTTACAATCAA TATCTCTTAATTGTATTAATTACTACT TGGCTTCTAAATTAGTTCCCTCT TAACAAGCAAGAAATGGAACAGG TAATATCTAAAATTAAGTAAACCC ATGGAATAGTTCTAGGACTCTGAC CAAAGCTT	Induced in Individual 10, repressed in Individual 9	NM_001759
174	A + AP3	clone RP11-120K22 on chromosome 6	182bp		Induced in Individual 1, but not in Individual 9	AL137178
175	G + AP41	Familial Cylindromatosis cyl gene	241bp		Repressed in Individual 11, but not in Individual 12	AJ250014

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
176	G + AP41	ribosomal protein L8 (RPL8)	218bp	GGCATAAACACAAACTTTATTGAGGCCCTCAGCACTAGTTCTTCTCC TGACAGTCTGGTTCCCGGAGA CGTCAGTCGGGGGGAGCAAT GAGACCCACCTTGCAGCCAGCG GTCATCTCGGGATGGTGGAGG GCTTGGCGATGTGCTGGTGGTGC CACCTCCAAAAGGATGCTCCACAG GATTCATGCCACACCCGTAAGCTT	Induced in Individual 11, but not in Individual 12	NM_000973
177	G + AP42	No significant match to anything	241bp	GATACTAAATGGTTTGCCAGCAA AAAGGAGTGAACCTACTCTTAAAA CACCCGAGTAACCAAGCTGCTACT AAGACTAGAGGGATGCTAACTAACAA GCAAAAGTCAAAGGTACTAACAA ATTAGCTAAGATTATACTTTGCA GAAAAGTCAATTCAAGGTAAATTCCG CTATTATCCCTGTGTATTATTC CTAAATAACTGGCAATTCCACCTTA AACTACGGTGCAGCTT	Repressed in Individual 11, but not in Individual 12	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
178	G + AP42	cDNA FLJ10589 fis, clone NT2RP2004389	330bp	GAAACTAACATTCTTATTTCC TATTTTAAAGTCACCTTACAAA GTAGCATTAAAATAAATCCATCT CACAGCTCAAAGAAATTCTGACAG TACTGCCCTCATGCTGGTCAGCCA TTATTTACTGTGTCTGCCACATG TCGGCACATATAAGCTCTTCT CTCCCTTCTCTGGAGCAAACCCCT AGCGTTCTCCACGTAACCTTCT GGGGCTCCCTCTGGCTGGCTT CTTCGGTTCCCTCACACGTGGATC AGTAGTAAGTAGTCAGCTTGCTC ATCCACTGACCTGTCCTGGTG CAAAGCTT	Repressed in Individual 11, but not in Individual 12	AK001451
179	G + AP47	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D)	217bp	GCCGGTCTCAGTCCTTAATCGTGG CAGGGCCCTCACGCCAGGGCAC GTACACACACTCAGGCTTCAGATC TTGGAAAGCTGCAGATATGACA CTCTGCACGTGCTCCCTCAAACTTG GTGATCTCCCTCCAGCAAGCT GTCCCCACCTTGTGCTCCACC ACACACTGAATCTGAGCTCCGG ATACCGTAGCCCACGGGATAAGC TT	Repressed in Individual 11, but not in Individual 12	NM_001960

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
180	G + AP47	Chromosome 16 BAC clone C17987SK-A-67A1	270bp	GATTCAAGGGTCTCGTTATGTCACCT AAGCTACAGTGCAATGGCACAAATC ATAGCTCAACACAACCCCTGAGTTTC TGGGCTCAAAGGATCCTCCACT CAGTCTCTAGAGTAGCTAGGACAT CAGGAGGTGCCAACAAACCTAGC TTTTTTTTTTTTTANATATA AGTCCCACACTAGGTTGCCCTGGCTG GNCTTAAACTCTGGTTTCAAGTGA TCCTCCTGCCTGGCCTTCCAAAAT GCTGGTATTACGGCATAAGCTT	Induced in Individual 5, but not in Individual 12	AC004531
181		No insert - just vector				
182		No insert - just vector				
183	A + AP41	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7) (PSMB8)	451bp	AGCTTACGGGGTCAATGGACAGTGG CTATCGGCCATACTTAGCCCTGAA GAGGCCTATGACCTGGCCGAGG GCTATTGCTTATGCACTCACAGA GACAGCTATTCTGGAGGGCTTGTCT AATATGTAACCACATGAAGGAAAGAT GGTTGGGTGAAAGTAGAAAGTACA GATGTCAGTGCACCTGCTGCACAG TACCGGGAAAGCCAATCAATAATGG TGGTGGTGGCAGCTGGGCAGGTC TCCTCTGGGAGGTCTGGCCGACT CAGGGACCTAAGCCACGTTAAGTC CAAGGAGAGAAGAGGAGCTAGCCCT GAGCCAAGAGAGAGTACGGGCTC AGCAGGCCAGAGGAGGGGGTGAAT GTGCATCTTCTGGGTCTCTATT TGAACAAAGCATTCCCCCAGGGAA GTTCTGGGTGCCCACTAAAGTAG AATAAAAGAAAAACGGTTAT	Expression is higher in Individual 5 and Individual 11 then in Individual 12	NM_004159

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
184	G + AP42	lectin, galactoside-binding, soluble, 9 (galectin 9)	153bp	AAGCTTTGCACCGTGCACCAAACCC TTACCCCTCTGGAAAGCAGGCC TGATGGCTCCCACTGGCCTCCAC CACCTGACCAGAGGTCTCTCA GAGGACTGGCTCCCTTCAGTGT CCTTAAATAAAGAAATGAAAATGCA TTGTTGGC	Repressed in Individual 5 and Individual 11, but not in Individual 12	NM_002308
184	G + AP42	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	201bp	GACTATCTACAAAAATTATTATA TTTACAGAAGAAAAGCATGCATAT ATTAAACAAATAAAATACTTTTATC ACAACACAGTACATATTGTCAATT TTTAAAGCCACACAATAGAAACAA GACACCAAGATAATTAAATTATCTG TTGACTCCGTAAATAATAGCTAAACA CTCATCATCGCGGTGCAAAGCTT	Repressed in Individual 5 and Individual 11, but not in Individual 12	NM_000938
185	A + AP47	Chromosome 16 BAC clone C1T987SK-A-67A1	106bp	AGATATGAAAGTCCCACCTAGGTT CCCTGGCTGGCTTAACACTCTGG TTCAAGTGATCCTCTGCCTGG CCTTCCAAATGCTGGTATTACGG GCATAAGCTT	Induced in Individual 11, but not in Individual 12	AC004531
186	A + AP46	UbA52 gene coding for ubiquitin-52 amino acid fusion protein	103bp	ACACGACTGAGGTTTACTCCAGTTTACAGATGACAAATCCAGAGTCA GGGGCATAGGGCAGGGACCAAAT CGGATGTGACAGAATCTAGGACCG AAGCTT	Slightly induced in Individual 11, but not in Individual 12	X56997

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
187	A + AP44	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) (SNRP70)	206bp	<pre> AAGCTTCTCGGGAGAAATGGGTATT TGATGGAGGGCTGCCGGGAGTGA AGGGTCGTCCCTCCATCTGCTG TGTTGGACGCGTTCCTGCCATCTGCTG CCCTTGCTGTCAATCCCCCTCCCCA ACCTTGGCCACTTGAGTTGTCT CCAAGGGTAGGTGTCTCATTTGTT CTGGCCCTGGATTAAAATAAAA ATTAAATTCTGTT </pre>	Induced in Individual 11, but not in Individual 12	NM_003089
187	A + AP44	isocitrate dehydrogenase 3 (NAD <sup>+</sup> ) gamma (IDH3G)	204bp	<pre> AAGGCACAAACATCTGAAGGCCATCC AGGACGTCATCGGCCACATCCGGC TCATCAAACGGCCGGCCGTGGAG GCCTAGGTGGCCCTAGGACCTTC TGGTTTGTCTTGGATTTCCCTT CCCACTCCAGCACCCAGCCAGCC TGGTACGCCAGATCCCAGAATAAAG CACCTTCTCCCT </pre>	Induced in Individual 11, but not in Individual 12	NM_004135
188	A + AP44	no insert - just vector		<pre> AAGCTTGGAGACTGGCTGGCAA CATGGAGAACCCATCTCCACTA AAAATACAAAAAAGTGGATGGCAT CTGGCGGGCAACTGTAATCACC CTAATCGGGAGGCTGAGGCCAGAAG ATGCCCTTGAACCCAGCAGATTGCAC TGTTGCAGTGAGCCAGATTGCAC TATTGCACCTCCAGCATGGGTGACG GGGCAAGACTCGTCAAAAACAAA CAAACAAAACGATAATAAATC </pre>	Repressed in Individual 11, but not in Individual 13	AL049715

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
190	A + AP52	hypothetical protein FLJ20436 (FLJ20436)	204bp	AGGGAGGTGCTAGTACAGAGGA ATCCCTTTATGATCAACTAGAGCT GGTCCTTCACTTCAGTCGAGTG CTGTCTCATTAGACACAGTAAG AGTTAACAGGTACCAATGGCAGT CGCATCTTCTGGTAAGGCAGTG TCTGGTCATTGGAAAGAGACTGATT GGAAACAACGAACATCATCCACAAA GGTCAAGCCT	Induced in Individual 11, but not in Individual 13 or Individual 5	NM_017822
191	G + AP49	c-Cbl-interacting protein (CIN85)	317bp	AAGCTTAAAGTCCATAGTGGTACTAT TTTGATGATAATTTCAGATTCAATTAAAAA TGTAATTTCAGATTATCGTTACAA GCCTTATAATTTTATGATTTTTAAAT CGTGTGTTGTCACAGACTCCCTAG TGTTTGACTACACGTAGTCAGAAG CGAGTGTCTTTCTTTGCTTCAG GCTAAGAGCTGCCTCGCTCTTGT CCCCCATTATGATTCTATTACATA TGCAATTGAGGTCAACCTGTC TTCCCTGCCAGCAAACCCACCA CCCTAAGAGAAATTAGCTTATAT ATGACGGTATATTAC	Repressed in Individual 11 and Individual 5, but not in Individual 13	AF230904

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
192	G + AP49	ribosomal protein L7a (RPL7A)	293bp	GGCTGAAGGAAATTGTATTATT CAATTATTTATGTACAGAAAACT CAACAGTGTACATTAACCCAGTT AGTGGCAAGTCTTAGCCTTGCCT TTTCGAGCTGGCATAACGAGCC ACAGACTTAGGACCCAGGACATTG CCACCCCAGTGACGGCGGATCTCA TCGTATCTGTCAATTGTGTC TGATAGCTTCCACCAAGCTTAGCCA AAGGCCTTGTCTTCCGAGTTCA CCTGTGTGAAGGGCGACAGTGGTC AGGTCTTCTGTGGACTAAAGCTT	Induced in Individual 11, but not in Individual 13	NM_000972
193	G + AP51	ribosomal protein S21 (RPS21)	318bp	GGTAGGTTTCATTATTTATGAA CAAATATTCCACATCTGTGATTCTC TCCAGTCAAAAGTTCTTGAGACGA TGCCATCGGCCCTGGCCAATGGGA GAATGGAATCATCTGACTCACCCAT CCTACGAATGGCCCCGGAGATAGC ATAAGTTTAAACTGGCCATTAAAC CTGCCCTGTGACCTGTCAACCTCG GCCACGTTCATCTGGATGGATGCG TGGTCCCTGGCACCGATGATGCGA TGGCTAGGGAGCATTTCCGGGC ACGTACAGGTCCACGAACTCGCCG CGGTGTTCTGCATTGAAAGCTT	Induced in Individual 11, but not in Individual 13	NM_001024

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
194	G + AP50	Chromosome 16 BAC clone C1T987SK-A-67A1	150bp	AAGCTTTGAGACTGGAAAGGTAC GCTGCTGCCAGCATGGAGAAGA AGCTGCTGAGCATGGCTTCCTGTA GTCTTTAGCAAGACACAAGTGATT TTGACTTTGTATCATGTCTATGATT CTAACAATAATGATGTTTTATGT GCC	Induced in Individual 11, but not in Individual 13	AC004531
195	G + AP50	sorting nexin 6 (SNX6)	132bp	AAGCTTTGAGACTAACCAAAGTATT GTAAAAATAACAGCGATAACAGTGA TAGTTTTAACTCTATGGTCATGT ATCACTCTGGAAAATGTGGAGTAG CTGTAATAATCTACTCCTGTATTAA TGCTTTAC	Repressed in Individual 11, but not in Individual 13	AF121856
195	G + AP50	No significant match to anything	133bp	AAGCTTTGAGACTATGTACAAATAC ACTAAAGTGGTGAATGGTGTCAATA TTGTNAAGGAATTATTCTGATAAAAT GAGAAAACGGATAATAATGTCAAAT AAGCTATTCTCAATAAAATCTC AAATCTC	Repressed in Individual 11, but not in Individual 13	
196	G + AP50	TNF-inducible protein CG12-1 (CG12-1)	87bp	GGTGAGTAGGTGAGTTATTAGGA CTTACACACAGGGCACTCAGCAGG ATGGCTCTAGAGATCCGGCCCTCC CCAGTCTCAAAGCTT	Repressed in Individual 11, but not in Individual 13	NM_014349
197	G + AP50	BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA	55bp	GTATTTTAGTAGAGATGGGTTC ATCATGCTGCCAGGCTAGTCAAAGCTT	Repressed in Individual 11, but not in Individual 13	Z75887 Z75888
198	G + AP51	ribosomal protein S24 (RPS24a)	160bp	GAAGTTTTAGTTATAATGTTCTT GCGAAAAATCCACAGTGGCCACAG CTAACATCATTGCAGCACCTTACT CCTTGGCTTTGCAGCCCCCAA CATTGCTTCAATTCTGTCTTGCCTTA ATTTCGAAAGCTT	Repressed in Individual 5 and Individual 11, but not in Individual 13	NM_001026

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
199	G + AP51	No significant match to anything	120bp	GGCATCTGGGTTACTATACTCACT CATGCCAAATCCAAGGTAGTGAAT GGAAAACAATTGGTAAATAGATG TTGGGCTATAAGCATCCTCCCTTA TATTAGACATTCGAAGCTT GGAAACTGAATAAATTAAACCTTTA TTACAAAAAGCAAAATGTTAGTTTC TCATTGTAAGTGATTCAAGAAAAACA ACGGTAACAGCCCCCTGGCAGGAGCT GGGACCAGGATACCAAGTATGCAGG CTGAGGGTCAAAGGTCAAAGCTT	Repressed in Individual 11, but not in Individual 13	
200	G + AP52	CGI-128 protein mRNA	146bp	AAGCTTACGGGGTGTGCCATGAA TCCTGTGGAGCATCCTTTGGAGG TGGCAACCACCGCACATGGCAA GCCCTCCACCATCCGAGAGATGC CCCTGCTGGCCGCCAAAGTGGGTCT CATTGCTGCCGGGAACCAAGACTGTGAC TCTCCGGGGAAACCAAGACTGTGAGG GGAGAAAAGAGAACTAGTGTGAGG GCCTCAATAAAGTTGTGTTTATGC C	Induced in Individual 11, but not in Individual 13	AF151886
201	G + AP41	ribosomal protein L8 (RPL8)	218bp		Induced in Individual 11, but not in Individual 13	NM_000973
202	G + AP41	Familial Cylindromatosis cyld gene	241bp	GGCAAAACATCACAGAAATAACTG TTCCAGATTCTATTGTTTCTCCAC CTTCAAAAGAAACTCTGGAGTTATT TCCAAAGGAGGAAGTGTGACCTGC ATTGTGTCCTCAGGTCTAGTTGTCCAA TCACCTTTCAAATGCAAGTCATCAT CTTCTATGAGTTCTAGTTGTCCAA TGGAAACAAACACGCCACAAATCTCA TCACACTGAAAAGCTGTTCCTT GGTACACCCCGTAAGCTT	Repressed in Individual 11, but not in Individual 13	AJ250014

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
203	G + AP47	Tu translation elongation factor, mitochondrial (TUFM)	358bp	GGCTTACTATTCAAAGTTACTGAC CTCCCAGGCCAGGGCCAAACC CTTCGAGCGGGGAAATGTCCAT CTAGCTGCCCTCTGCTGGGTTGCA GCCTATGCCATGAGAGGGTACTGG AAGCAGGAGGGAGGCCCTGGCTAG GGCAGGGCTTAAACGCAAGGGAAAG Induced in Individual 11, but not in Individual 13	NM_0033321	
204	G + AP47	KIAA0787 protein	200bp	CCCCATTGGATAATTCTCCCTCCT CTGAGCAGAGATCTGCACACTCAA CCCCATCTGGCATGGCTGTTGGTGA CAGTCATGCCAGGCCAGGTGTTGGT CTAGACCGGTGCCAATAGTCCGGT TGCCATCTCGCAGGGTGAAACGCT GGCCTTTCTCTAAAGATCATTGGCTG CCGCAAGATTAGGTGAACCTCAN GTCCCTCCCCGGGCAATAAGCTT AAGCTTATGCCGATGCTCTCTGTT CATTCCCGACCCCTTCTACTATGCA TTTCCCTTTATCAGGGTATAAAG TAAATACTGTGTATTATTCACTAAA AAGTACATGAACCTTAAGAGACAAC AAGCCTTTCTGTGTTTCCACAGGT GTTAACGCTTCTGTACAGTTGAA ATAAACAGACAGCAAATGGTGC Induced in Individual 11, but not in Individual 13	AB018330	
204	G + AP47	ribosomal protein L13 (RPL13)	203bp	GATTCCAAGTCCCCAGGGGGCTT TATTTTCCTTTCAACATCCGTTC TGCGGCTTCTGGCTCTTTGCT CGGTATGCCGAAGGGGGGACTAG GGCACGGGGCATACGGGAGACTAG CGAAGGGCTTGAAAATTCTCTCTC CTCAGTGTATGACTCGAGCTTCTC CTTCCTTATGACGTTCCGGACGGG CATAAAGCTT	Induced in Individual 11, but not in Individual 13	NM_000977

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
204	G + AP47	fatty acid synthase/ NY-REN-57 antigen RNA	202bp	GGAGATCACATGGGGTTAACGTGGAGGGCTGAGAGCAGCATTTACCAAATTGGTGTAAAGAAGCGGGTCCAGACGTGTACACTGACAGTTACAGTAATTTCAAAATCCAAGCAGCAATTGAATCATTCITGAAAAACAAACACAGACAAACACCAAACATGGAGTTGGTGCCTGGCGGGGCATAAGCTT	Induced in Individual 11, but not in Individual 13	S80437
218				AAGCTTATGCCCGCAGGTCTAAGACCAAGGAAGCACGCAAGGCCGTGAAGAGGCCCTCCAGGCCAAGAAAGAGGAGATCATCAAGGACTTTACCAAGGAGGAAGAGACCAAGAAATAAACCTCCACCTTGTCTGTACATACTGGCCTCTGTGATTACATAGATCACCCATTAAAATAAAACAAAGCCTTAACTCTGC	Induced in Individual 11, but not in Individual 13	NM_000981
204	G + AP47	ribosomal protein L19 (RPL19)	198bp	GGAAGGAATAATTCTAAATGATAAGATATGCTCTGGCTACACAGCACAAATAAAAGATGGTTTAGCTTACATGATCTGATTGTCTGTCAAACAAAGAATCCAACAGTTCAAGGCTCTGACACGTCCTCTTCAAGCTAGGGTGTGCAAGATGTTATGGAATCATCACCCCTCATAGTCAGCCAAAGCTT	Repressed in Individual 11, but not in Individual 13	AL078584
205	G + AP45	clone 245M18 on chromosome 6p21.32-22.3	186bp			

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
205	G + AP45	clone TCBA00781	184bp	GAATGTCCAAATTGTTTATTAGT ATGAAATTACAAAACCTTACTTAT TAGGGTAACGGTGGAGCTGGAGA GTATTGGCCTCTCAAGCTGCC CGGCAGAGGCCACCAAATAGTGTGG TGAACCTGGCCCCCTCCAAAGG CACGGCTCTTGGCCGTGAGAT GTCAGGCCAAGCTT	Repressed in Individual 11, but not in Individual 13	AF283772
206	G + AP45	chromosome 19, cosmid R26529	198bp	AAGCTGGCTGACGTTATGGTGGC TTCAAGCTTCACTAGGAATGGGACA CAGGGCTGGGGCCTGTGACTCC CACACCCCAGGGCCTGGGTAGGG ACAGGGTGGTGGTCCCTGGGTGG GTCAAGGTAGGGCACAGGGCCAG GGAGGGACAAGCAGACCTCAAGG CGCTGCCAGATGGAATAATTAAATT ATTGTTGGCC	Induced in Individual 11, but not in Individual 13	AC005551
207	G + AP47	tumor suppressing subtransferable candidate 1 (TSSC1)	182bp	GGAGGGTGGATTATTATTTCAT TTTTACTCTCAAGAGAAAGAAGAG TTACTACTGCAGGAACAGACATT TTAAAAAGCGAAAACCTCTGACACC CTAAAAACAGAAAACATTGTTATTC ACATAATAATGTGGGGCTCTGTCTC TGCGGACAGGGCTGGTTGGG CATAAGCTT	Induced in Individual 11, but not in Individual 13	NM_003310
208	G + AP43	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	74bp	GGTTGAGGCACAGGGTACTTTATG ATGGTACATGACAAGGTGGGCTC CCTAGGGCCCTCCGGCTCAAGCTT	Induced in Individual 11, but not in Individual 13	AF261085
209		no insert - just vector				

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
210	G + AP52	transferrin receptor (TFRC)	105bp	GCACATAACAGCTTTATACAATGA TAAGGACATATCATTGTTACAA GAAAGTCTAAAATTCAAGAACATT CAAAGAGCTAACACAGTAAGGTC AAGCTT	Induced in Individual 11, but not in Individual 13	AF187320
211	G + AP55	Homo sapiens PAC clone RP4-649M7 from Xq23	287bp	GTAAATTGTTGAGTTCATGGTAG ATTCTGGATATTAGCCCTTGTCAAG ATGAGTAGGTTGTGAAAATTCTCTC CCATTGTTGAGTTGTGCCCTGTTCACT CTGATGGTAGTTCTTTGCTGTGC AGAAAGATCTTAAAGTTAAATTAGATC TCATTGTCAATTGTTGTCTTTATTG CCGTTGCCTTGGTGTGTTGGACAT GAAGTCCTTGCCTATGCCATATGCC CTGAATGTAATGCTTAGTTCT TCTAGGGTTTATGGTTTATGTC TAACGTAAGCTT AAGCTTTGAGGTTACATGATATGC	Induced in Individual 11 and Individual 5, but not in Individual 13	AC006968
212	G + AP54	ubiquitin-conjugating enzyme E2D 3 (UBE2D3)	142bp	TTTATGCTCATAACTGATGTTGCTG GAGAAATTGGTATTGAAATTATAGCA TCAGCAGAACAGAAAATGTGATGT ATTTTATGCAATGTCATAAAAGGAAT GACCTGTTCTGTTCTAC	Induced in Individual 11, but not in Individual 13	AF224669
212	G + AP54	putative DNA-directed RNA polymerase III C11 subunit	142bp	AAGCTTTGAGGTGAAGGCCAGG GGGTCAAGAAATAGGCCTATCTG CCAGGCAGGGTGGAAGTCATG AATGTCGGGGAGTTCTGTGTTGG GGAGGGAGACAGAGACCCATAACTA AATATGCTCTGTGAAAGTCC	Induced in Individual 11, but not in Individual 13	AF126531
213	G + AP54	testis-specific kinase 2 (TESK2)	89bp	AAGCTTTGAGGTACAAAGTAAGAA GGCTGACCGCACCTGTAACACTG ACTTTATTTTAAGTCTGAAAATGTC TTGGGAAAAGTTTAC	Induced in Individual 11 and Individual 5, but not in Individual 13	NM_007170

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
213	G + AP44	integrin, beta 2 (antigen CD18 (p95))	87bp	GTAAATAAATTGGCACCCACCTTAA TCAGACTGATGTCCTGACTTGAC AGGAAACAGGCACCTAACCTCACC AACCTCAAAAGCTT	Induced in Individual 11 and Individual 5, but not in Individual 13	NM_000211
214	A + AP49	No significant match to anything	111bp	AAGCTTTAGTCCACTTACAACAAA GAGCAGCTGTCTTGCAGCCTTGT TAGCTCTAAACTCCAGATTAACCT GTGTAGCCATTCACTAGCACTAAA AGATTAACCT	Induced in Individual 11 and Individual 5, but not in Individual 13	
215	G + AP49	PAC clone RP4-726N20 from 7q32-q34	139bp	AAGCTTTAGTCCAAATTAGGGAGTAA AAGGAGGGAAAGGGGCCATTCATT CATTGGAAAGCTGGCCAGGGTG CGAGGACACTCTCCCTCAGGGAA ATATGTTATGTGGAGGGAGCAAT AAATTATTTTTTTCC	Induced in Individual 11, but not in Individual 13	AC006344
216	G + AP49	BAC R487K10 of library RPCI-11 from chromosome 14	133bp	GGGGAGAAATGTATCAAAGGAGT TTATTTAAAGCAATGGTAGTATCAG TCCTAAAGCAAAACTGGAACAAAAA TAAAAAACACAAAAACCTTTCTCGG ATATGAAATCATCGATTATGGGA CTAAAGCTT	Induced in Individual 11, but not in Individual 13	AL352976
217	G + AP49	F-box protein FBL4 mRNA	100bp	AAGCTTTAGTCCATAATATGATTGA TAAGAAATAACATGGAAATCATGCT AACTTATTTCAAAGGAACACTGAG CAATAAAAGTATCGTGGCATTATGC	Repressed in Individual 11, not in Individual 13	AF176699

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
218	G + AP11	cDNA DKFZp762H1311	215bp	AAGCTTCGGGTAAGGGATGAGAAC TCTGAAATCAGATGGAAAAGAGCG GTGTTAATTTCATGGTCTGTGATC GTAGCTGTATAAGGGACTGAGGA ATAAATTGTCCTGCTGAAAGGCCCACTGA ACCAGCTCTGTCCTGCTGGTAAC AAATTGCCGTCTGCCTTAA GCTACGGGGTAAGATTGCCACC CAGTACTATTTCTGCCACC	Repressed in Individual 5, not in Individual 13	AL359617
219	G + AP4	cDNA DKFZp434F2021	63bp	GGCTTCAACTACATGTCAGGTGTTA ATATGAAAAATCTGCACAGCCTAC CGTTGAGAAGCTT	Repressed in Individual 5, not in Individual 13	AL117573
220				GGTATGTTTTAGCAGCACTCTTTT TTCATCAAWATGGATTATTTAAATT TTAGATTTAAATTGTGTTAATAAAA AGCCCTCATTCATGAGGGCTTTATT TTATGGATGATAAAATTGCTTAACCG TGACGTTTGCAAACACTGTTCCATGA ATTAAACCAATGCTTGACCCCTTC TAAAGGCACAGCAATTGAAATAACTT GCACGCATACCCACAGAGCGA TAAGCTT	Repressed in Individual 5, not in Individual 13	
221	G + AP19	No significant match to anything	233bp	AAGCTTATGGCTCATATAATGAGGCAT CATATATCCCTCTCACTCTGGAC ACCATAGCCACTGCCCTCCCT GAATGCCAGTAATGTTATGTC TACT GGTGGGAGACTGTGAGGATCCCC GGATTCA GTATTCCCTGGCCAGAG GCCCTTGCTGGCTACTGGGTGTT AGTTTGCA GTCTGTTGCTTCCC TCTCTTATGACTGTGTCCTGGTTG TCAATAAAATATTCCCTGGC	Repressed in Individual 5, not in Individual 13	NM_006156
221	G + AP19	neural precursor cell expressed, developmentally down-regulated 8 (NEDD8)	239bp			

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
222				AAGCTTCACTAGCTGACTAATAAA GAAGAAAAGANAAAAGATCCAAATA AACACAATTAGGAATGACAAANGG GATATTACCGNTGACGCCACAAA ATACAAATAACCATTACAGACTATG ACACACCTCATGCACAGAAACTAGA ATTCTAGAAGAAATTGGATAAATT CTGTACAAATNCATCCTCCATACT GAACCCAGGAGGAATTGGATNCNT GAACAGACCAATAATGAGCTCTNA ATGGAATCAGTNATNAATAGCCTA CTACC		
223	BAC C-2149C7		276bp		Induced in Individual 5, but not in Individual 13	AL132827
224		Rattus norvegicus mitochondrial cytochrome c oxidase subunits I, II and III, and ATPase subunit 6 genes	173bp	AGGATCCTCATCAATAGATAGAAC GTATAGGAATAGTCAACTACATCT ACGAAGTGTCAAGTATCATGCTGCG GCTTCAAATCGAAATGTATGTTTG ATGTGAAGTGGAAATTTAGTTGTCG TAGTAGACAGACAAATTAGGAAAGTT GAGCCAATAATTACGTGGAAGCTT	Slightly repressed in Individual 11, but not present in anyone else	M27315
225	A + AP10	cytochrome c oxidase subunit III gene	116bp	AGGGGGGGCTTCGAAGCCAAAGT GATGTTGGATGTAAGTGAATAAT TAGTTGGGGATGAAGCAGATAGT GAGGAAAGTTGAGCCAAATAATGAC NTGAAGTACGTGGAAGCTT	Induced in Individual 11 and Individual 5, but not in Individual 13	AF004341
226		No insert - just vector				

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
227		No significant match to anything	322bp	GAGGTTCAACTTAACCATTTATTGCAACATCACCTCAGGCCACTGCTGACATCCAAAACACAGGCCTAGTAA CACACAACCTCACCTCAAGGACTGCAGAGATAAACCAACTATATAA ATAATCTCGTGGAAACGTAATTGG GTGAGAAANAATATGACGCTAGAGA CTTTCGCGATGAATATTTCGCTTAAG TTCAGAAAGCTGGAAAATACAGTTGG CCTACAATCTCAAATTTCACCCAAAT AACCGTGCCCTTAGTCACCACAC CTTCCATCATCTTTACCTCTGCC TGTTCCTGCCCTTACAGTCGAAGCTT	Induced in Individual 10, but not in Individual 9	
228		No significant match to anything	136bp	AAGCTTCGACTGTACATCATGAAATAATCCTAGGGATCTACTGTATACTATAGTGACTATAGTTAGTGATACTGT ATAGCATACTGGAAAATTTCGAG AGGGTAAATTACATTAAGTGTTC TTATCTGCC	Repressed in Individual 10, but not in Individual 9	
229	cDNA YI27F12		127bp	AAGCTTCGACTGTAGTACCCCTTCAATGGCATTACTACCAATAGCCTAT TTGTTATTGCCCTCAAGCTCCATTAGGCAAATTGTTTTCAATTGTTTAAAGTCAGCACCTAAATCTCCCTGGCC	Repressed in Individual 10, but not in Individual 9	AF075018
230	G + AP2	ribosomal protein L8 (RPL8)	66bp	GGCATAAAACACAAACCTTATTGAGG CCCTCAGCACTAGTTCTTCTCC TGACAGTCGAAGCTT	Induced in Individual 10, but not in Individual 9	NM_0000973

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
231	G + AP4	CGI-51 protein mRNA	371bp	<pre> GTGTCCTTAAACATTTATTGACGGGG TTTCCCACAGGGTCCGCAGTCAAA GAATCGCTNGAACGGGGTTCCCTC GAGAGACGGGTGTGGCATGGGC GCCCTTGCTGCTGCCCGAGTCCAG AGCTTCTCTGTAGGGGGTCCGGC TACAGGAACCTTATCCAGCTCCA ACTGGACGCCATCACATCCCTG TCACCTGTCGTGACTCCATGGGG ACGCAGTAATTAAAGTTCCAACCGA GCGATGTTGCCAAGCCTGAGGACA ATCCCCGGCCCGTAGCACCAGCG GATGCACTAGGCCAGCTTACGAAT ATGAGCTTGGGCCCTCCCCATA GTTGAGGTTGCAGAGGTTCCCTGC GTTGAGAAGCT </pre>	Induced in Individual 10, but not in Individual 9	AF151809
232		BAC clone RP1-35D2 from 7q21.1-q21.2 or cosmid U107D4	228bp	<pre> GCATAGGATTGACTGGCAATGGG GGCTCTTTTGGTTCCATATGAAC TTAAAGTAGTTTTCCAATTCTG GAAAGAAAGTCATTGGTAGCTGA TAGGGATGGCATTGAATCTAAAT TACCTGGCAGTGGCCATTTC ATGATATTGATTCTCTATCCATG AGCATGGAAATGTTTCCATTGTT TGATTCCTCTTATTCGTTGAGA AGCTT </pre>	Repressed in Individual 10, but not in Individual 9	AC006374

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
233	G + AP4	ALI1-fused gene from chromosome 1q (AF1Q)	212bp	GGGATTGAAATGTCTTTTATAAATAA ACGAGTAAATGGTAGCACAAATCA CCATCAAATTTTGAAAGGATTGG GGACAAGATGTCGAGTCAGAATAT AATTGTTCAATTTCAGGGTCTCAATG TAGCTGAAGAACACTGTGCCCACTGA TCAGTATTACGTATTGCAAATGCAG GAGGTAAGGGCTAAAATAGGACTTA TGCCGTTGAGAAGCCTT AAGCTTCAATTCCGGTACTCAATTGC TCCCTTAAGAGTATCAATATTCTGG CATCACAAACAGATAACAGTATTCTAT TGTTTTTTCAACTCAATTGTAAA ACTTTGGAGAGAAAGGAACCATAAA TTTTTGAGAATATACAAACAGAGAT ATTCCACAAAGAACATAATGAAAGCA AGACTCACATGCACATACCTATGTA TAAAAGAACACCTACATAAATTGAA TTAAGGAAGGAGGCCCCGGGT GGTGGCTCACACCTGTAATCCCAA CACTTTGGAGGTCCGAGGAAGGGT GATCACCTGAAGTCAGGAGATCGA GACCATCCGGCCAACGTGGTGA ACCCGTCTTCACTAAATAC	Induced in Individual 10, but not in Individual 9	NM_006818
234	G + AP9	BAC R-11K13 of library RPCI-11 from chromosome 14	365bp		Repressed in Individual 10, but not in Individual 9	AL355095
235		Insert is too small		AAGCTTGAAGTGCCTAGGCCAGA AAATTACATTAGCATCCTCTGGT AAATTACATTAGTTAGGTGTCCTC CC	Repressed in Individual 10, but not in Individual 9	AL132777
236	G + AP12	BAC R-307P22 of library RPCI-11 from chromosome 14	76bp			

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
237		clone RP3-505P2 on chromosome 6	281bp	AAGCTTCACTAGCTAGAGTAACAA GAAAACGAGAGACAAAAAGATCC AAATAAGCACAATGAGAAATGACAA AGGCCAATATTGCAACCAATACCCACA GAAATACAAAGGTCTCGAGAC TATTATCAGACACCTCATGTGCACA AACTAGAAAATCTAGAGGAATGGAA TACATTTCTGGAAAGCACACAACTCT CCAAGATTGAATCAGGAAGAAATT GAAACACCCTGAACAGAACAAATATCAA GTTCCCAAACCTTGAATCAGTAATAAA AAACCTAC	Repressed in Individual 10, but not in Individual 9.	AL133458
238		No insert - just vector				
239	A + AP5	No significant match to anything	93bp	ACAAGGGAGTCATTTCACATTG CATTTGTCAGAATAATAGACCGAA CTTCCCATTCTACAAGACACTTGAT TGAGTGCCTACTAAGCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	
240	A + AP10	No significant match to anything	241bp	ATAAAGGGCCAGATAGTAGCTGTG GGCTGGGGCTCTCAAACCTGTGTTGC CCACTACTCAACTCTGCCATTGTA TGTGAAAGTAGTCACAGACAAATA TAAGAAAATGAGTGTGACTGTGTT CAAAAAACTTATTACAAAGCA TCAGTGGGCTGGATTGGCTTT GGGCCATAATTAAATCCCTCTGG NAAAATAATCACTATTAGCTGG TCATGAGTACGTGGAAAGCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
241	A + AP10	cytochrome c oxidase subunit III gene	183bp	AAGACCCTCATCAATTGATGGAGA CATACAGAAATAGTCAAACCAACATC TACAAAATGCCAGTATCAGGGGG GGCTCGAACGCCAAAGTGATGTT GGATGTAAGTGAAATAATTAGTGG CGGATGAAGCAGATAAGTGAGGAA GTTGAGCCAATAATGACCGTGAAG TAGGTGGAGCTT	Induced in Individual 10, but not in Individual 9	AF004341
242	A + AP19	The size of this gene does not match the autorad	91bp	AGTAAGGGGACAGAAGGGACCTCT GAGGAGGGAAGATAGGGAGTTGA AGCCTGAGCATTAAAGTTCTCTGG AGTGGGAGGCATAAGCTT	Repressed in Individual 10, but not in Individual 9	
243	A + AP19	ribosomal protein S7 (RPS7)	346bp	ACTGTGAATATACTTTTATTAG TCATTTTGTACAAATTGAAACTCT GGAAATTCAAATTAAACATCCTCTGC CCGTGAGCCTCTTATAGACACAG AAAAAGTTCAACCTTGTGTTCCAC ATTGTTCTGCTGTGCTTTGTCCAAA TGAACCTTTATGAGC GGCTCTGC CTACAATTTCGCTTGGAAAGACCA AGTCCTCAAGGATGGCATCGTGC CAGCTGTCAAGTAGCTGGCTCCTGG GACGCTTTGCTTATTGTTGTACG GCTTTTCGAGTTGGCTTAAGCAGA ATTCTCCTCTGAGGATAAAAGCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	NM_001011

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
243	A + AP19	No significant match to anything	392bp	GCTTATCGCTCCTAGGCTACAAAC CTGGCACAGCATGTTCACCGTACTGA AGACTGTAGGCAGTTGTAACACAA TGGTAAGTATATGTGATCTAAATA TATCTAAACATAGAAGAGGTAAATGC ATTGCACTATAAACATTACCTTATGA CAGGCCACGACATCTCTAGGTGACA GGAATTTTAGCTCTATTAAAGTT TCTGGGATCACCAATTCTATATGTGA TCCATCATGACTGAAATGTCAATT TGCGAGCAAATTGTATATAACTATT TCCATTGGCTCTGCCTAAAAATCTT AGTAGTGTGGCAGAACCTGGATA GGGATTGTTAAGGCCATATGGTC AAGCATATGAAATTTCGATATTAT GTTTATGGAAAGACTCCTTTGT	Gene is repressed in Individual 10, and not expressed in Individual 9	
244	C + AP17	No significant match to anything	125bp	AAGCTTACCCAGGTAGGAGAAAATA CTAGAAAAGCACAGCTCCCTGGAG TAGTGGAAATGAATCTATCATCAATA CCATTCCCTACAGTTTCTGCAATT AACATGGTACAGTAGGCCAACAAATT GG	Gene is repressed in Individual 10, and not expressed in Individual 9	
245	C + AP17	clone CTA-732E4 on chromosome 22q12.1	86bp	CAACATTGGAAACAGGAAATAAA CCTCCCTTATTTATCTCCTCTC TATCTTGAACATCTGGCATAGTACCC TGGTAAGCTT	Repressed in Individual 10, but not in Individual 9	AL008722
246		Insert is too small				
247	C + AP20	UBA3 (UBA3) mRNA	133bp	CACAAATATGATTATTAAAT AGTGCAAAAGCATCAGTGATAACT GTTTGAACATTAAATTAAACAG CCATGTCCTGGCATTAGTTAATT GTGCATATTGGCCTATGGCACA ACAAGCTT	Induced in Individual 10, but not in Individual 9	AF046024

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
248	C + AP21	No significant match to anything	92bp	CCAAAAAGAGGCCATGCCAGAGGG AAAGTTGAAACGAAAGCCAAGTT TTCATTAAAAGGAAACATTAAGA GGTTAGCCAGAGAAAGCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	
248	C + AP21	hypothetical protein (HSPC004)	96bp	CACGGAAACCAGATACTTATTAA ATCTACTCTTAGCCGAGCAATAAG ATGTCTACAGAGTTACAACCTGCA ACACTTCACCAACAGAAAGCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	NM_015918
249	C + AP23	Homo sapiens 12 BAC RP11-575G13	207bp	ATAGAATGATGCAATTGGACTTCA GGACTTGAGGGAAAGAGTGGAG GAGGTGAAGGATAGAAAGAGTACAA ATATGGTGCACTGTAACTGCTG GGTGATGGGTGCACCAAATCTCA TAAATCACCACTAAAGAACATTACT ATGTAACCAAATACCAACCTGTACCT CAATAACTTATGG	Gene is repressed in Individual 10, and not expressed in Individual 9	AC010200
250	G + AP41	Familial Cylindromatosis cylid gene (hypothetical protein (HSPC057))	241bp	AAGCTTACGGGGTACCAAGGG ACAGCGCTTTTCAGTGTGATGAAGA TTGTGGGTGTTGTGCATTGGA CAAGCTAGAACTCATAGAAGATGAT GACACTGCATTGGAAAGTGTATTAC GCAGGGTCTGGGACACAATGCAG GTCGAACCTCCCTGGAAATA ACTCCAGAGTTCTTGAAGGTGG AGAAACAATAGAATCTGGAACAGTT ATATTCTGTGATGTTTGGCC	Induced in Individual 4 and Individual 10, but not in Individual 13	AJ250014

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
250	G + AP41	ribosomal protein L8 (RPL8)	218bp	AAGCTTACGGGGCATGCCATGGAA TCCTGTGGAGCATCCCTTTGGGG TGGCAACCACCGCACATGGCAA GCCCTCACCATTGGCAGAGATGC CCCTGCTGGCGAAAGTGGTCT CATTGGCTGCCGGGGACTGGACG TCTCGGGGAACCAAGACTGTGCA GGAGAAAGAGAACTAGTGCTGAGG GCCTCAATANAGTTGTGTTATGC C	Induced in Individual 4 and Individual 10, but not in Individual 13	NM_000973
251	G + AP55	Homo sapiens chromosome 5 clone CTD-2165P17	136bp	AAGCTTACGGTAGGGCAGAAAAG AGAACACATTGGTCTCTATTCACA GTGGATTGACAAAGGTGTTCCGT AGGTAAATAATGTTTGGCTGAGAGA TGTCAAGTTAGCACAGGAAGCAACA CAGTGGGATTGGCC	Induced in Individual 4, but not in Individual 13	AC010411
252	A + AP47	No significant match to anything	240bp	AGCTAAATAACCATCATTATGTTAT TAAATAGAAGCCAATTCTACCTATG TCACTCTAAATTCTGATCTTGCAA TTCAACTGTTGGTATTACAATA ATTGTTATTATTCTAGACAGCAAGA ATAAAATAAAATAAAGTGGGTGAATGA TTACATTAAGACATTGTTCCCTAA GTAGTAATTAGGAAAAGGCTTAA TTAATAATTCCCAAGTCACCCC ACGGGGCAATAAGCTT	Induced in Individual 4, but not in Individual 13	
253	A + AP47	Chromosome 16 BAC clone CIT987SK-A-67A1	106bp	AGATATAGAAGTCCCACAGGTTG CCCTGGCTGGCTTAAACTCTTGG TTCAAGTGAATCCTCGCCTTGG CCTCCAAAATGCTGGTATTACGG GCATAAGCTT	Induced in Individual 4, but not in Individual 13	AC004531

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
254	A + AP52	hypothetical protein FLJ20436 (FLJ20436)	204bp	AAGCTTGACCTTGTGGATGATGTT CGTTGTTCCAATCAGTCCTCTCCAA TGACCAAGACACTGCCATTACCCAGA AAGATGCGACTGCCATTGGTGAAC TGTTAACCTTACTGTGGTCTAAT GGAGACAGCAGCACTCGACTGAAAGTG AGGACCCAGACTCTAGTTGAACCA TAAAAGGATTCCCTCTGACTAGCAC ACTCCCCT	Induced in Individual 4 and Individual 10, and only slightly in Individual 13	NM_017822
255	A + AP45	No significant match to anything	187bp	CCACAGAGTAATAAACTCATC ACACATTAAAAATACCTTCCAACT ACTTTTACATGACTTAATGTTCCA ATTATTTGCAGAAACCATGTCCCCGC AGGTCTTAGCTGGTCCTGTTAAG ATTCTTAATTTCATTTGCAATATC TAAATTTTATTTACATACATGTGGA CTAAAGCTT	Induced in Individual 4 and Individual 10, but not in Individual 13	
256	C + AP49	clone TCBA00781	223bp	AGTTTAATAGACATTTCCTCA GTTGAACACCTCTACACAATTAA ATGTATGACTTAAGATCTTTCTTT TTGTGAAGAAATTAGGTCTCAAG ACTTTTATGAACCTGCTATGAGTA CTTCCTGGAAATCAATTAACTGAGT CTTTGAAACCCCTAGAGAAGATAG GAGAAAATTGGTTCAAGAACGAGCA TTAAATTAAGTCAGCCAAGCTT	Induced in Individual 4 and Individual 10, but not in Individual 13	AF283772

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
256	C + AP49	No significant match to anything	225bp	AGACAAGAGCATTGCCAGATGTAC TGTGGATTCCCTTACCATGGCA AATTCCATAGTGATTTCATTAGA ACGATAAACACAATTGTTGCTTGA GATGAAAGGAAGGGCTTGCTTGA AGTGTGTTGGAGTTATAGTTT CACCTGCAGGAACATGTGGATT GAGACATATAGGAAGTGATTTTT TTCTGTGCTTTAGTCAGCCAAGC TT	Induced in Individual 4 and Individual 10, but not in Individual 13	M14483
256	C + AP49	prothymosin, alpha	224bp	AAGCTTGGCTGACAATGAGGTAGA CGAAGAAGGAAGAAGGGGG AGGAAGAGGGAGGAAGAAGAA GGTGATGGTGAGGAAGAGGGATGG GATGAAAGATGAGGAAGCTGAGTCA GCTACGGCAAGCGGGCAGGTGCA AGATGATGAGGTGACGATGTGCA TACCAAGAAGCAGAAGGACCGAGA GGATGACTAGACAGCAAAAAAGGA AAAGTTAACCT	Induced in Individual 4 and Individual 10, but not in Individual 13	
257	C + AP51	KIAA0874 protein	240bp	AAGCTTCGAAATGCTAGAAAAAT TGGAAATGGAGTATGCTGAAAA GGTTTGGATTCAAGAAAGAAAAAG GATGGTTAGTTAACATGATGATTCT TTTAAACTCTCAAATATCATGAA AAGATACTAAATTGTACCTAAGGAT TTGTATTTCCTTACAATTGTTCTAA ATATCTGTGTTAACATGACTTAGTTGATA TTTGTGCTATGGTTATTAAATAAGAG TTATATTTTATAG	Repressed in Individual 4 and Individual 10, but not in Individual 13	AB020681

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
258	C + AP49	(a total of 3 matches-equal scores for each) chromosome 5 clone CTD-2284O10, Homo sapiens mRNA; cDNA DKFZp434L1; Homo sapiens cDNA FLJ12597 fis, clone NT2RM4001371	86bp	CAACAGAAATAAATTATAATCCAGG AGATTCTGCCATTTCAGCCTGGAAAACGT GACTAAAGCTT	Induced in Individual 10, but not in Individual 13	AC0008925
259	C + AP53	No significant match to anything	185bp	AAGCTTCCCTCATGTTAACACAAAC AAATGCAAATGTAGCTCTGCCTCCC TCCCTCCTATAGTAACACTAAA ACCATATTCAATACATATGATT GAAAATGAGATTATAACCTGCATT TTTACTTAAACAATGTATATTGCGA CATTTTGATGCCGTGTACAGAGAT CCTCATATG	Induced in Individual 4, but not in Individual 13	
260	C + AP56	mRNA for KIAA1618 protein, partial cds	192bp	AAGCTTATGAAGGACAGGCACAGC TGTGGACCGATTGCAAGTACAGGG AGAAAGAGGTGAAGAGATAACCTGT GGCAACATCTGAAAAAACACGTTG TACCATTTGCCCTGTGGACTGCC CGGACTTTTGCAAGCAGGAAAGCA CAGTGAGGAGTAAACTGAAAACAG GCCTGATTGTCCTTTGTAGTGG	Induced in Individual 4 and Individual 10, but not in Individual 13	AB046838

*Table 11*  
*Class Discriminator Genes*

GENE	t-test p-value
5-aminoethylutidate synthase 2 (ALAS2)	0.0010
Cide-B (CIDEB)	0.0006
clone RP11-468G5	0.0008
metallothionein-1G (MT1G)	0.0040
NADH oxidoreductase subunit MyoFE	0.0030
Penicillin Band 109-A-2	0.0003
Penicillin Band 117-B-2	0.0050
Penicillin Band 134-A-2	0.0031
Penicillin Band 134-A-4	0.0046
Penicillin Band 149-B-3	0.0037
Penicillin Band 239-A-2	0.0016
Penicillin Band 240-A-4	0.0000
Penicillin Band 244-A-2	0.0001
Penicillin Band 69-B-3	0.0031
Penicillin Band 77-C-2	0.0041
prolymosin, Alpha	0.0049
Rat mitochondrial cytochrome c oxidase I, II, III, and ATPase subunit 6	0.0029
ribosomal protein S21 (RPS21)	0.0014
ribosomal protein S24 (RPS24)	0.0028
ribosomal protein S4, X-linked (RPS4X)	0.0008
ribosomal protein S7 (RPS7)	0.0018

**CLAIMS**

1. A method of identifying hypersensitivity in a subject, the method comprising:
  - 5 obtaining a gene expression profile of genes associated with hypersensitivity of a subject suspected to be hypersensitive; and detecting in the gene expression profile of the subject a predetermined pattern of gene expression of genes associated with hypersensitivity.
- 10 2. The method of claim 1 wherein the pattern of gene expression associated with hypersensitivity is obtained by comparing the gene expression profile of a hypersensitive individual with the gene expression profile of an individual who is not hypersensitive.
- 15 3. The method of claim 1, wherein the genes associated with hypersensitivity comprise at least 2 genes associated with hypersensitivity.
4. The method of claim 1, wherein the genes comprise at least 5 genes associated with hypersensitivity.
- 20 5. The method of claim 1, wherein the genes comprise at least 10 genes associated with hypersensitivity.
6. The method of claim 1, wherein the gene expression profile of the subject that is obtained comprises a profile of levels of mRNA or cDNA.

7. The method of claim 1, wherein the gene expression profile comprises a profile of levels of protein expression.

8. The method of claim 1, wherein expression of the genes predetermined to be associated with hypersensitivity is directly related to prevention or repair of toxic damage at a protein, nucleotide, macromolecule, organelle, tissue, organ or system level.

9. The method of claim 1, wherein the gene expression profile is a profile of nucleic acid expression obtained from a cell or tissue sample, or a protein expression profile derived from cells, tissues, blood, urine or serum.

10. The method of claim 1, wherein the gene expression profile is obtained from a blood, urine or serum sample.

11. The method of claim 1, wherein the method comprises identifying hypersensitivity in the subject to an agent.

12. The method of claim 11, wherein the agent is a pharmaceutical agent.

13. The method of claim 11, wherein the agent is selected from the group consisting of pharmaceutical agents listed in Table 1.

14. The method of claim 1, wherein the genes comprise genes associated with tissues or cells within the digestive system, comprising the liver, pancreas, intestines, colon, rectum, stomach, gallbladder, kidneys or bladder.

15. The method of claim 14, wherein the genes are genes associated with liver toxicity including altered lipid metabolism, fatty liver, cholestasis, jaundice, hepatitis, steatosis, necrosis, hyperplasia, mutagenesis, tumor formation or peroxisome proliferation.

5 16. The method of claim 1, wherein the genes are genes associated with tumor formation, teratogenesis, immunosuppression, pancreatitis, or agranulocytosis.

17. The method of claim 1, wherein the genes are genes associated with cellular manifestations of toxicity.

10

18. The method of claim 17, wherein the plurality of genes comprises genes associated with apoptosis, cell adhesion, autophagocytosis, cell cycle arrest, circadian rhythm, cytokine release, de-differentiation, differentiation, mitochondrial damage, migration, mutation, oncosis, peroxisome proliferation, recombination, senescence, signal refractivity, spreading, or transformation.

15 19. The method of claim 1, wherein the plurality of genes are genes associated with renal toxicity.

20

20. The method of claim 19, wherein the genes comprise genes associated with, necrosis, glomerulitis, nephritis, tumor formation, hyperplasia, proteinuria, renal damage or renal failure.

25

21. The method of claim 1, wherein the genes are genes associated with cardiototoxicity, blood toxicity, skin toxicity, eye toxicity or neurotoxicity.

22. The method of claim 21, wherein the plurality of genes comprises genes associated with tachycardia, arrhythmia, hypotension, hypertension, leukemia, neutropenia, agranulocytosis, peripheral neuropathy, dementia, inflammation, irritation, sensitization, myelosuppression or retinopathy.

5

23. The method of claim 1, wherein the genes associated with hypersensitivity are associated with a specific ethnic group, sex or age group.

24. The method of claim 1, wherein the genes are selected from the group consisting of the genes listed in Tables 3, 4, 5, 6, 8, 10 and 11.

10 25. The method of claim 24, wherein the genes comprises at least 5 genes.

15 26. The method of claim 1, wherein the genes are selected from any one of the group consisting of the genes listed in Table 4.

27. The method of claim 26, wherein the genes comprise at least 5 genes.

20 28. The method of claim 1, wherein the genes are expressed in one or more different cell types within a single tissue or organ.

29. The method of claim 28, wherein the tissue or organ is selected from the group consisting of liver, kidney, lung, heart, pancreas, muscle, brain, testes, ovaries, spleen, stomach, intestines, colon, rectum, eye, and bone.

25

30. The method of claim 29 wherein the cell types are selected from the group of liver cells consisting of Kupfer cells, sinusoidal cells, ito cells, hepatocytes, bile duct epithelial cells, hepatic venule endothelial cells and sinusoidal epithelial cells.

5 31. The method of claim 28 wherein the cell types are selected from the group consisting of the cells listed in Table 9.

32. A method of identifying a number of genes associated with hypersensitivity to an agent, the method comprising:

10 comparing the gene expression profile of cells treated with the agent with the gene expression profile of cells not treated with the agent; and

determining the genes that have altered expression due to exposure to the agent in the treated cells, thereby to identify the genes associated with hypersensitivity to the agent.

15 33. The method of claim 32, wherein the cells comprise cells of one or more different cell types, and wherein each said cell type comprises a gene associated with hypersensitivity to the agent.

20 34. The method of claim 33, wherein said cell types are derived from a single type of tissue or organ.

35. The method of claim 34, wherein said cell types are derived from an organ or a tissue selected from the group consisting of kidney, liver, lung, heart, brain, spleen, thyroid, bone, muscle, intestine, stomach or skin.

25

36. A method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent, the method comprising:

comparing a gene expression profile of one or more cell types of a subject known to be hypersensitive to the agent with the gene expression profile of said cell types in an individual known not to be hypersensitive to the agent; and

identifying the genes from said one or more cell types having a pattern of differential gene expression, wherein the pattern of differential gene expression is associated with hypersensitivity to the agent.

- 5 37. A method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent, the method comprising:
- 10 comparing the gene expression profile of one or more cell types of a subject known to be hypersensitive to the agent before treatment with the agent with the gene expression profile of the one or more cell types of the subject after treatment with the agent; and
- 15 identifying genes from said cell types having a pattern of differential gene expression, wherein the pattern of differential gene expression is associated with hypersensitivity to the agent wherein the samples of multiple individuals are compared in at least six individuals and wherein the results of gene expression profiles are compared statistically using computer software.

- 20 38. An array for the identification of a gene expression profile indicative of a hypersensitivity to an agent, the array comprising at least 25 different gene probes, each probe comprising a nucleic acid sequence of a gene associated with the hypersensitivity to the agent, wherein said gene is selected from the group consisting of genes listed in Tables 3, 4, 5 and 6.

- 25 39. An array of claim 38 wherein the array comprises at least 100 different gene probes.

40. An apparatus for identifying hypersensitivity in a subject comprising:  
a detector for obtaining a gene expression profile of a number of genes associated  
with hypersensitivity of the subject suspected to be hypersensitive; and  
a second detector for identifying in the gene expression profile of the subject a  
5 pattern of gene expression of the genes associated with hypersensitivity, thereby to identify  
hypersensitivity in the subject.

41. The method of claim 11, wherein the method comprises identifying  
hypersensitivity in a subject to multiple agents administered together.

10

42. A method of determining hypersensitivity of a subject to an agent, the method  
comprising:

15

obtaining a cell from a subject;  
culturing said cell to obtain a cell culture;  
exposing said cell culture to an agent;  
obtaining a gene or protein expression profile of a cell or cells of said exposed  
culture; and  
detecting in said gene or protein expression profile a predetermined pattern of  
expression associated with hypersensitivity to the agent.

20

43. The method of claim 42, wherein the subject is a human being.

44. The method of claim 42, wherein the expression profile of at least 20 genes  
or proteins is obtained.

25

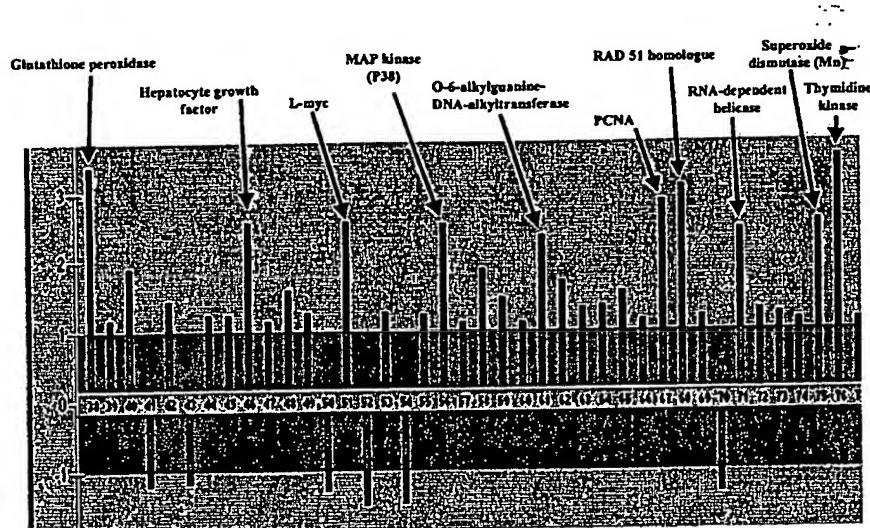
45. The method of claim 44, wherein the expression profile of at least 50 genes  
or proteins is obtained.

46. The method of claim 42, wherein the cell obtained from the subject is a leukocyte.

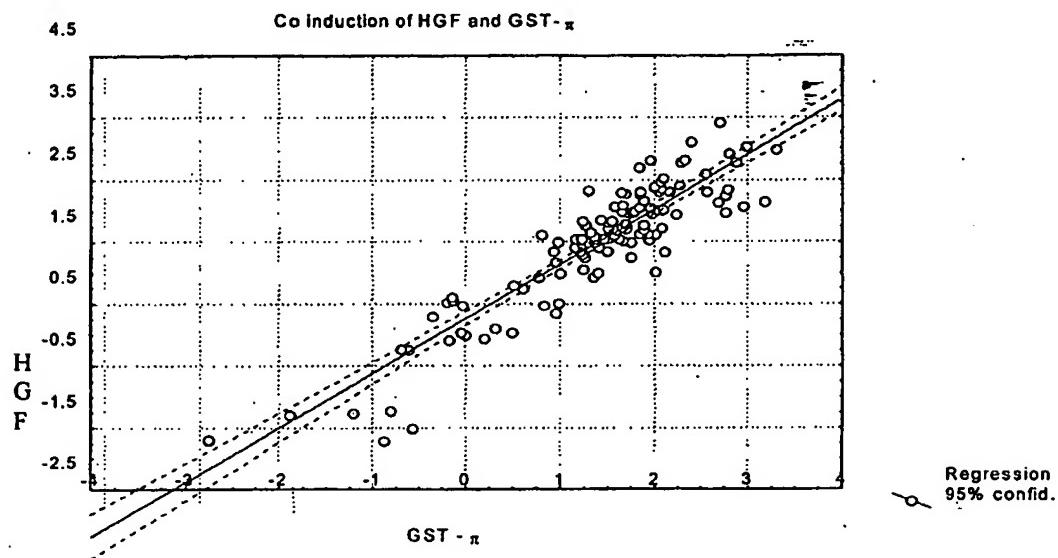
5

**FIGURE 1**  
**GRAPH OF GENE EXPRESSION CHANGES ASSOCIATED WITH TOXICITY OF**  
**GENOTOXIN STREPTOZOTOCIN**

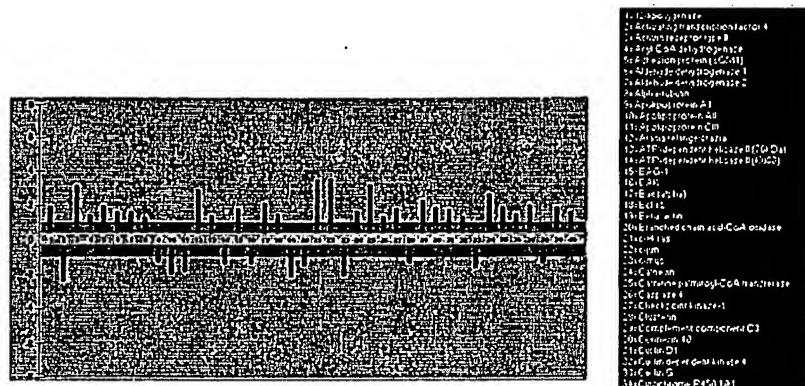
Gene expression profile from HepG2 cells treated with 480 µg/ml streptozotocin



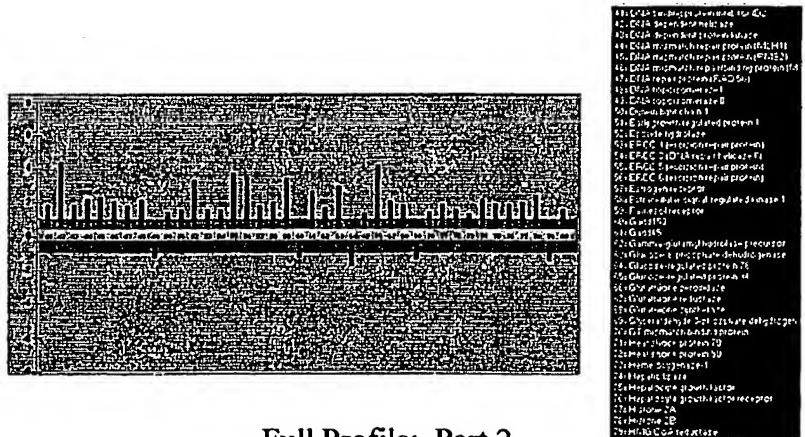
**FIGURE 2**  
GRAPH ILLUSTRATING THE COINDUCTION OF GLUTATHIONE  
TRANSFERASE AND HEPATOCYTE GROWTH FACTOR RECEPTOR GENES



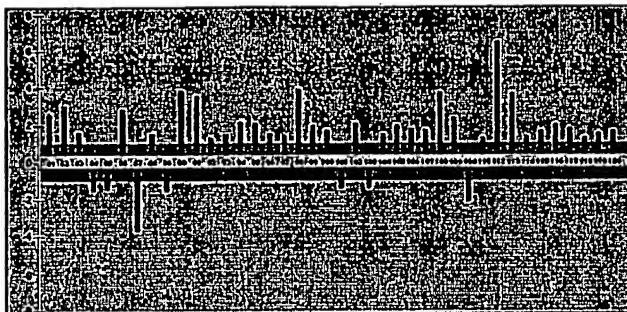
**FIGURE 3**  
GRAPH ILLUSTRATING THE GENE EXPRESSION PROFILE FROM HEART  
MUSCLE AFTER EXPOSURE TO THE CARDIOTOXIN, DOXORUBICIN



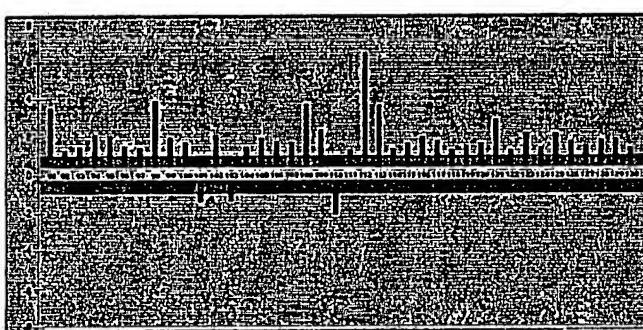
## Full Profile: Part 1



## Full Profile: Part 2

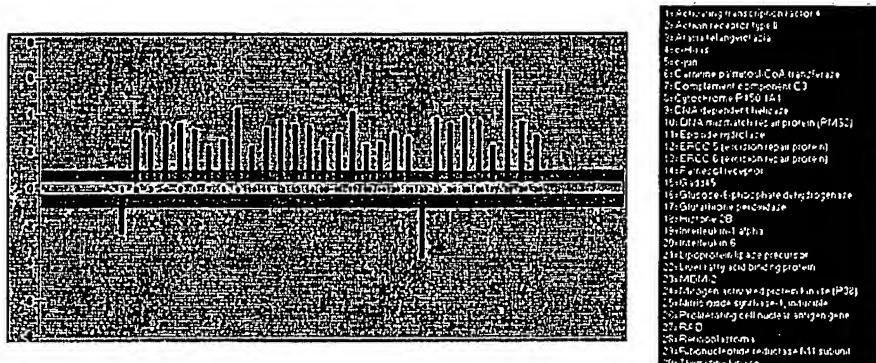


### Full Profile: Part 3



## Full Profile: Part 4

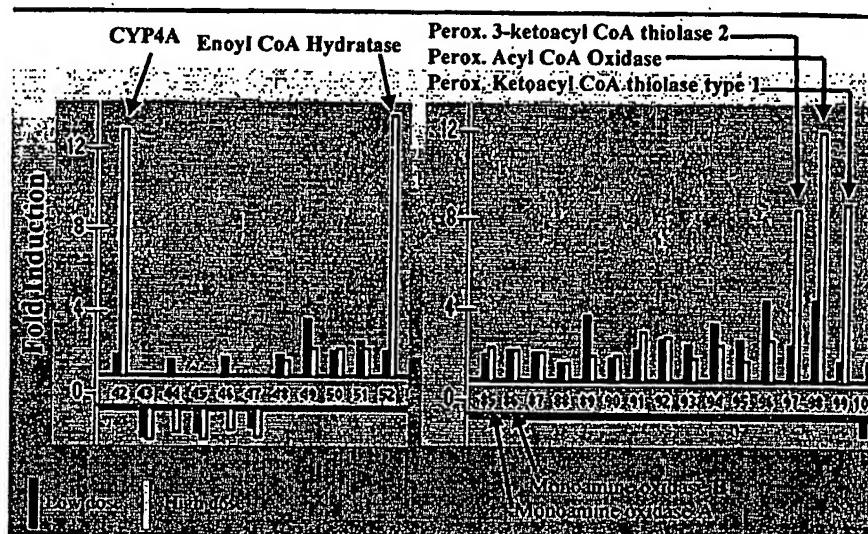
93: Histidine activated protein kinase (P-16)  
94: Histidine kinase domain  
95: Histidine kinase domain  
96: Histidine kinase domain  
97: Histidine kinase domain  
98: Histidine kinase domain  
99: Histidine kinase domain  
100: Histidine kinase domain  
101: Histidine kinase domain  
102: Histidine kinase domain  
103: Histidine kinase domain  
104: Histidine kinase domain  
105: Histidine kinase domain  
106: Histidine kinase domain  
107: Poly(A) polymerase  
108: Prokaryotic elongation factor G (GTPase)  
109: PRF1  
110: PRF1  
111: Protein kinase C (PKC) domain  
112: Protein kinase domain (kinase domain)  
113: Protein kinase domain  
114: Protein kinase domain  
115: Protein kinase domain  
116: Protein kinase domain  
117: Protein kinase domain  
118: Protein kinase domain  
119: Protein kinase domain  
120: Protein kinase domain  
121: Protein kinase domain  
122: Protein kinase domain  
123: Protein kinase domain  
124: Protein kinase domain  
125: Protein kinase domain  
126: Urokinase type plasminogen activator (U-PA) domain  
127: Urokinase-type plasminogen activator receptor (UPAR) domain  
128: Very long chain acyl-CoA dehydrogenase  
129: Virtex domain  
130: Virtex domain  
131: Virtex domain



Highest Expressing Genes Only

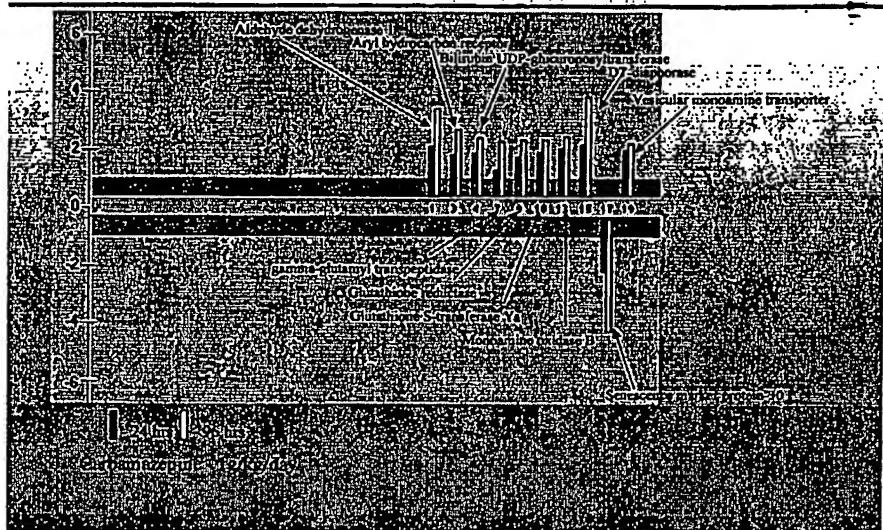
**FIGURE 4**  
GRAPH ILLUSTRATING THE GENE EXPRESSION PROFILE FROM LIVER  
TISSUE AFTER EXPOSURE TO THE HEPATOTOXIN, WY 14643

**Genes Induced in Rat Liver by WY 14,643**

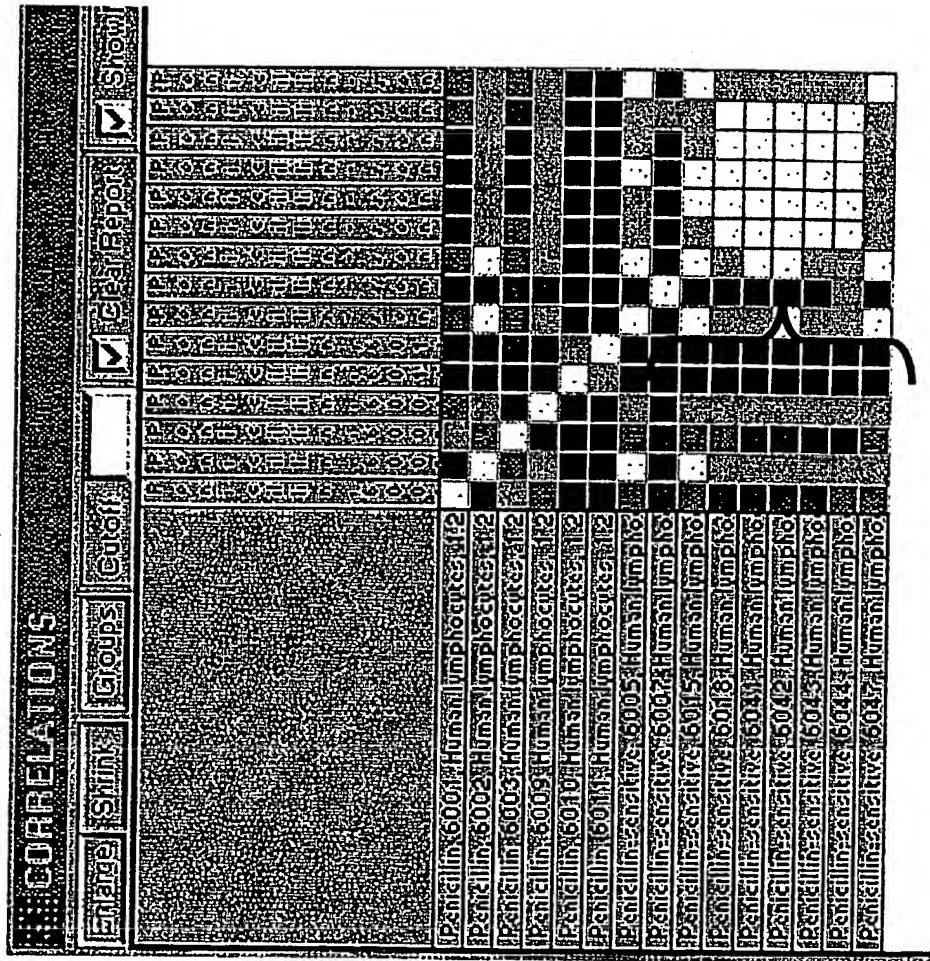


**FIGURE 5**  
 GRAPH ILLUSTRATING SOME GENES EXPRESSED FROM LIVER TISSUE  
 AFTER EXPOSURE TO THE HEPATOCARCINOGEN CARBAMAZAPINE

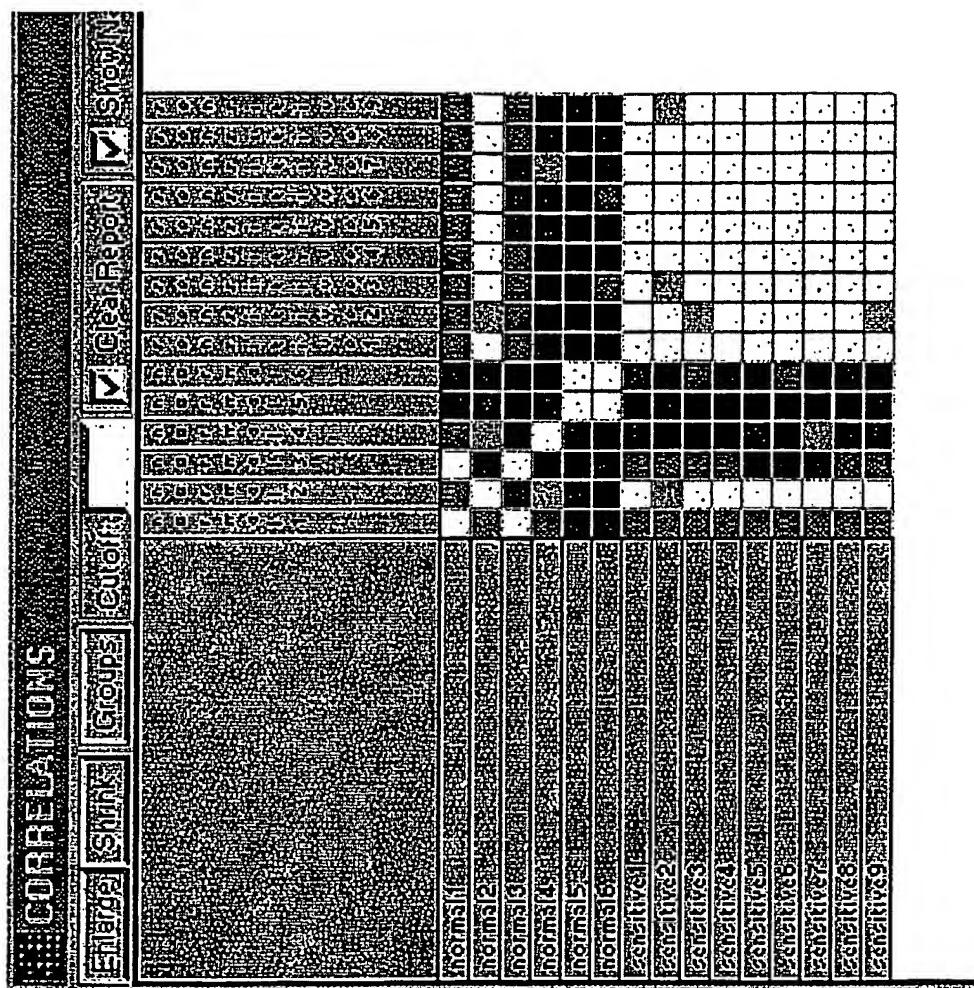
### **Genes induced or repressed by carbamazepine:**



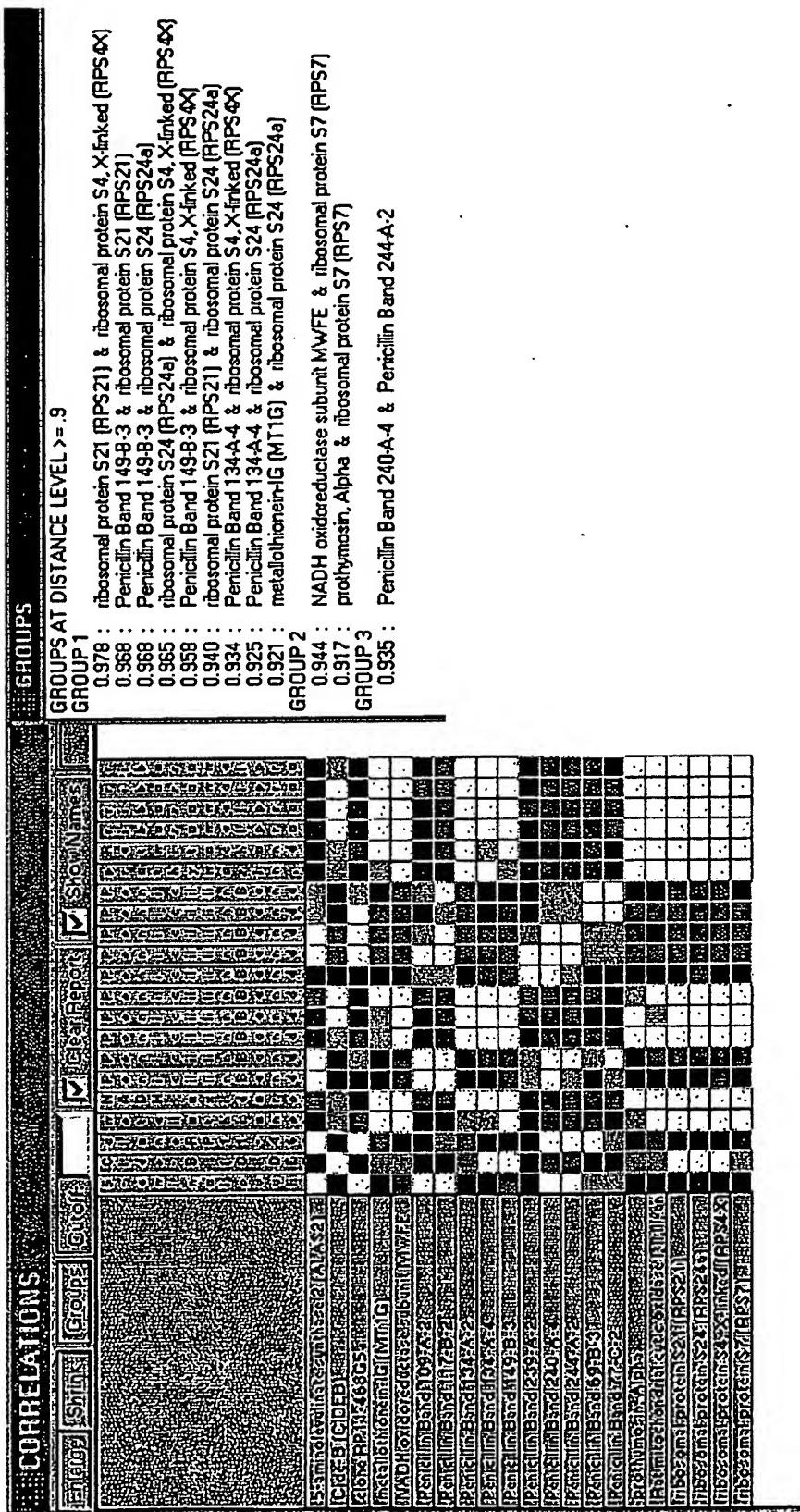
*Figure 6*  
*All gene correlation*



*Figure 7*  
*Discriminator Correlations*



*Figure 8*  
*Inter-Gene Correlations*



**Figure 9 Taqman Results with a Penicillin Sensitive Person**

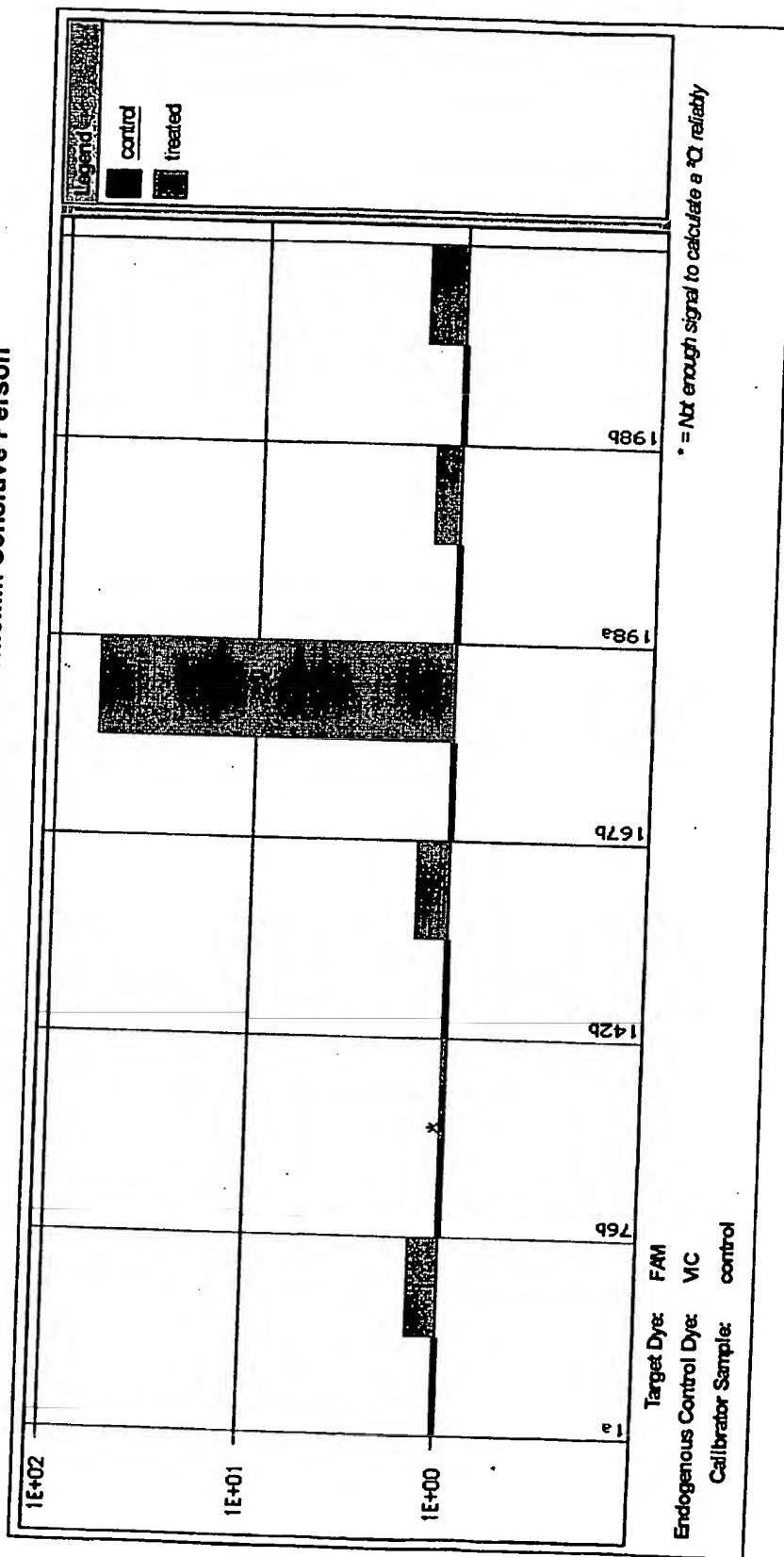
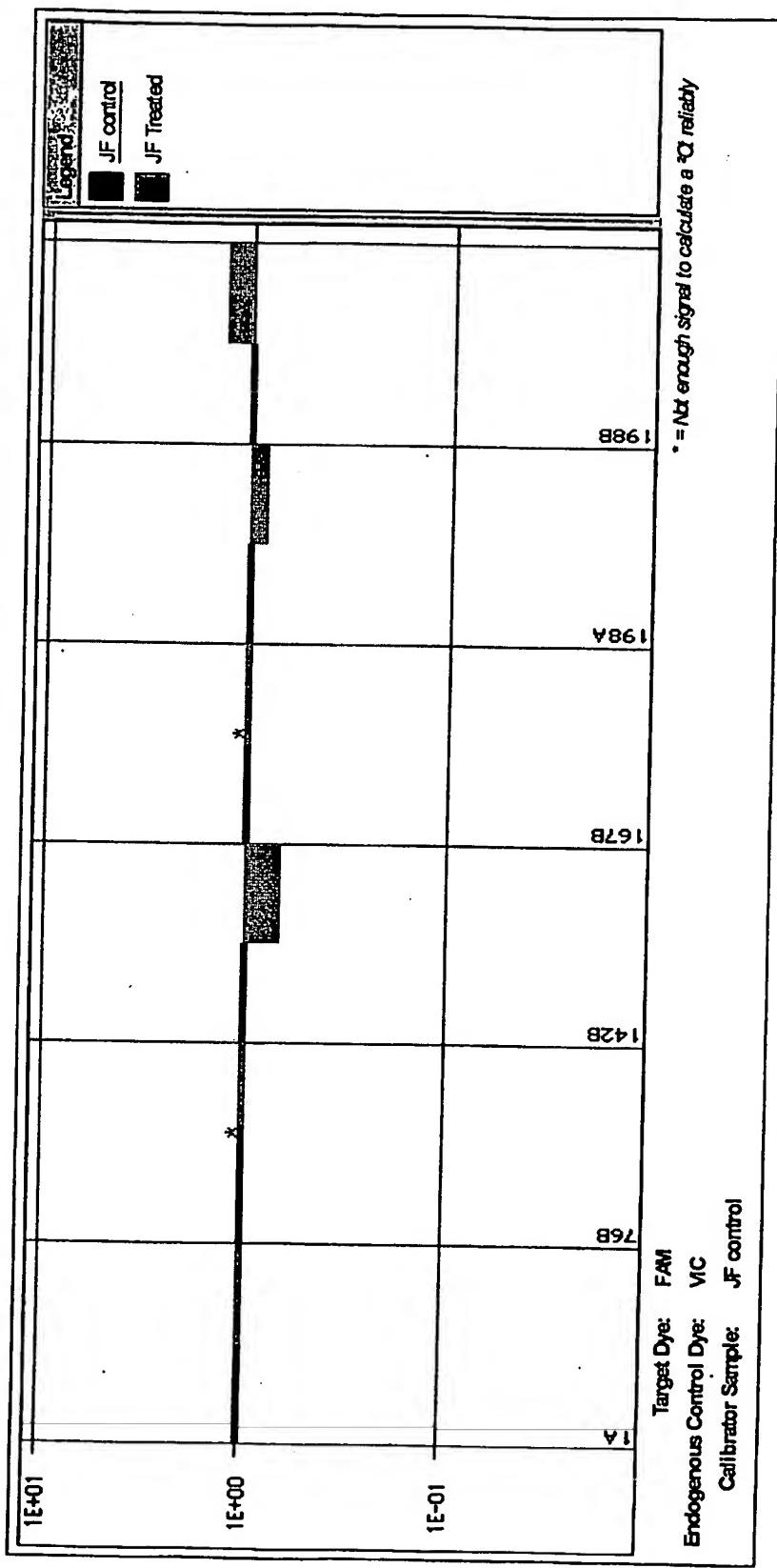


Figure 10 Taqman Results with a Penicillin Refractive Person



(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
10 May 2001 (10.05.2001)

PCT

(10) International Publication Number  
**WO 01/032928 A3**

(51) International Patent Classification<sup>7</sup>: C12Q 1/68, (81) Designated States (*national*): AB, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

G01N 33/50

(21) International Application Number: PCT/US00/30474

(22) International Filing Date:  
3 November 2000 (03.11.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/165,398 5 November 1999 (05.11.1999) US  
60/196,571 11 April 2000 (11.04.2000) US

(71) Applicant (*for all designated States except US*): PHASE-1  
MOLECULAR TOXICOLOGY [US/US]; 2904 Rodeo  
Park Dr. East, Santa Fe, NM 87505 (US).

(72) Inventor; and

(75) Inventor/Applicant (*for US only*): FARR, Spencer  
[US/US]; 2904 Rodeo Park Dr. East, Santa Fe, NM 87505  
(US).

(74) Agents: SHIEH-NEWTON, Terri, M. et al.; Morrison &  
Foerster LLP, 755 Page Mill Road, Palo Alto, CA 94304-  
1018 (US).

(81) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian  
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European  
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,  
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— with international search report

(88) Date of publication of the international search report:  
25 July 2002

(15) Information about Correction:

Previous Correction:

see PCT Gazette No. 20/2002 of 16 May 2002, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

A3

WO 01/032928

(54) Title: METHODS OF DETERMINING INDIVIDUAL HYPERSENSITIVITY TO AN AGENT

(57) Abstract: Methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes associated with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes associated with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes for the plurality of genes associated with hypersensitivity. The expression of the genes predetermined to be associated with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases arrays and apparatus useful for identifying hypersensitivity in a subject are also disclosed.

## INTERNATIONAL SEARCH REPORT

In  International Application No  
PCT/US 00/30474

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 7 C12Q1/68 G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
IPC 7 C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, MEDLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	EVANS WILLIAM E ET AL: "Pharmacogenomics: Translating functional genomics into rational therapeutics." SCIENCE (WASHINGTON D C), vol. 286, no. 5439, 15 October 1999 (1999-10-15), pages 487-491, XP002193947 ISSN: 0036-8075 page 487 -page 491; figures 1-3; table 1	1-46
Y	WO 99 23254 A (AFFYMETRIX INC ;NAIR ARCHANA (US); LOCKHART DAVID J (US); WARRINGT) 14 May 1999 (1999-05-14) page 1, line 8 -page 2, line 16 page 3, line 26 -page 4, line 3 claims 1,6-14	1-46

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

## • Special categories of cited documents :

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

22 March 2002

Date of mailing of the international search report

04/04/2002

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel: (+31-70) 340-2040, Tx. 31 651 epo nl.  
Fax: (+31-70) 340-3016

Authorized officer

van Klompenburg, W

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/30474

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 99 37662 A (MILLENNIUM BIOTHERAPEUTICS INC) 29 July 1999 (1999-07-29) page 84, line 23 -page 86, line 31 -----	1-46
A	US 5 807 680 A (ERLANDER MARK G ET AL) 15 September 1998 (1998-09-15) column 7, line 58 -column 8, line 58; claims 1,29-31 -----	1-46

## INTERNATIONAL SEARCH REPORT

Int'l Application No
PCT/US 00/30474

Patent document cited in search report		Publication date		Patent family member(s)		Publication date
WO 9923254	A	14-05-1999	AU EP JP WO US	1287799 A 1027456 A1 2001521753 T 9923254 A1 6033860 A		24-05-1999 16-08-2000 13-11-2001 14-05-1999 07-03-2000
WO 9937662	A	29-07-1999	US AU CA EP JP WO	6197551 B1 2562299 A 2318727 A1 1051427 A1 2002501078 T 9937662 A1		06-03-2001 09-08-1999 29-07-1999 15-11-2000 15-01-2002 29-07-1999
US 5807680	A	15-09-1998	US US US US US AU AU AU AU AU AU AU CA EP FI JP NO WO	5459037 A 6030784 A 6096503 A 6110680 A 6309834 B1 687127 B2 1055195 A 718304 B2 6711098 A 2174966 A1 0726946 A1 962000 A 9509306 T 961902 A 9513369 A1		17-10-1995 29-02-2000 01-08-2000 29-08-2000 30-10-2001 19-02-1998 29-05-1995 13-04-2000 09-07-1998 18-05-1995 21-08-1996 10-05-1996 22-09-1997 12-07-1996 18-05-1995

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

CORRECTED VERSION

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
10 May 2001 (10.05.2001)

PCT

(10) International Publication Number  
**WO 01/32928 A2**

(51) International Patent Classification<sup>7</sup>: C12Q 1/68. (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

G01N 33/50

(21) International Application Number: PCT/US00/30474

(22) International Filing Date:  
3 November 2000 (03.11.2000)

(25) Filing Language:

English

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(26) Publication Language:

English

(30) Priority Data:

60/165,398 5 November 1999 (05.11.1999) US  
60/196,571 11 April 2000 (11.04.2000) US

Published:

— without international search report and to be republished upon receipt of that report

(71) Applicant (*for all designated States except US*): PHASE-1 MOLECULAR TOXICOLOGY [US/US]; 2904 Rodeo Park Dr. East, Santa Fe, NM 87505 (US).

(48) Date of publication of this corrected version:

16 May 2002

(72) Inventor; and

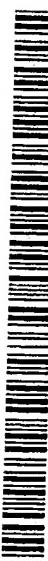
(75) Inventor/Applicant (*for US only*): FARR, Spencer [US/US]; 2904 Rodeo Park Dr. East, Santa Fe, NM 87505 (US).

(15) Information about Correction:

see PCT Gazette No. 20/2002 of 16 May 2002, Section II

(74) Agents: SHIEH-NEWTON, Terri, M. et al.; Morrison & Foerster LLP, 755 Page Mill Road, Palo Alto, CA 94304-1018 (US).

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



**WO 01/32928 A2**

(54) Title: METHODS OF DETERMINING INDIVIDUAL HYPERSENSITIVITY TO AN AGENT

(57) Abstract: Methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes associated with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes associated with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes for the plurality of genes associated with hypersensitivity. The expression of the genes predetermined to be associated with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases arrays and apparatus useful for identifying hypersensitivity in a subject are also disclosed.

**METHODS OF DETERMINING INDIVIDUAL  
HYPERSENSITIVITY TO AN AGENT**

**TECHNICAL FIELD**

5       The invention generally relates to methods, compositions and devices for identifying individuals who are hypersensitive to a given agent.

**BACKGROUND OF THE INVENTION**

Individuals exhibit a high degree of variability in their response to chemicals, 10 including pharmaceutical compounds. A major concern of pharmaceutical manufacturers is that a subset of the patient population may display significant toxic side effects that cannot be predicted from preclinical studies. In many cases this hypersensitivity results in extreme, and even lethal, responses. The incidence of serious and lethal adverse reactions to drugs among hospitalized patients in the United States causes at least 100,000 deaths per 15 year. This makes adverse responses to therapeutic drugs the fifth main cause of death in the United States.

The existence of a hypersensitive sub-population is usually only discovered after a compound has been broadly prescribed and a population base of sufficient size has had exposure to the compound. These same drugs are generally safe for the majority of 20 individuals and most respond favorably to the desired effects of the drugs. In many cases, the same drug that may elicit severe toxic responses in a subset of the population is the best drug for the particular disease being treated. For example, clozapine is a very effective drug for treating moderate to severe depression and with the majority of patients shows no toxic side effects at the recommended doses. Yet at the same dose (usually 300 mg), 25 approximately 1% of the patient population develop agranulocytosis, a severe blood disorder.

Many compounds have either been withdrawn from the market altogether or severely restricted in use due to severe adverse responses by a subset of the patient population. In some instances, it is known that a subset of the population is hypersensitive, and physicians are advised to be alert for indications of extreme toxic response in such patients. Exemplary compounds include tienilic acid, halothane, dihydrazine, diclofenac, fialuridine, carbamazepine, Trovan™ (trovafloxacin), Seldane™ (terfenadine), hismanol, dihydrolazine, warfarin, phenytoin, omeprazole, diazepam, haloperidol, perphenazine, perhexiline, phenformin, tolbumamide, penicillin, clozapine, aminopurine, quinidine and remoxipide.

Unfortunately, in the vast majority of these cases, there is no way of identifying a hypersensitive individual before prescribing the drugs or exposing the worker to the compound. Hypersensitive individuals are discovered the hard way; they exhibit toxic side effects that most people do not. Furthermore, since the mechanisms of toxicity are specific and usually different for each drug or compound, the hypersensitive populations are also different and specific for each drug or compound.

When an approved drug is found to elicit serious toxicity in only a subset of the population the manufacturer is usually required to tightly restrict access to the drug, carefully monitor all patients who receive the drug for toxic side effects, or withdraw it from the market altogether. A high number of compounds also fail in the late stages of development because of serious toxicity in a subset of the clinical trial population. When a drug is found to cause severe toxicity in a sub-population, besides the trauma and pain for such hypersensitive individuals, there is great financial loss incurred by the manufacturer. The cost to the manufacturer of withdrawing or restricting a compound can be billions of dollars in lost market capitalization, legal liabilities and unrecoverable research and development expenses. Adverse reactions are becoming the main challenge for pharmaceutical research and development. (Drug Discovery Today) 4:393-395 (1999). In

addition, very effective drugs are often pulled from the market and thus become unavailable to those who would benefit greatly from them.

It would save lives, decrease pain and suffering and save pharmaceutical manufacturers and consumers a great deal of money if there were a way to determine in advance which individuals were likely to experience severe toxic responses to a drug.

### SUMMARY OF THE INVENTION

Disclosed herein are methods, gene databases, gene arrays, protein arrays, and devices that may be used to determine the hypersensitivity of individuals to a given agent, such as a drug or other chemical, in order to prevent toxic side effects.

In one embodiment, the invention relates to a method of identifying hypersensitivity in a subject by obtaining the gene expression profile of specific genes associated with hypersensitivity of the subject suspected to be hypersensitive and identifying in the gene expression profile of the subject a pattern of gene expression of the genes associated with hypersensitivity. The gene expression profile of the subject may be compared with the gene expression profile of individuals who have an acceptable response and compared with other hypersensitive individuals. The embodiment also includes, for example, identifying hypersensitivity to an agent in a subject, where the agent may be a pharmaceutical agent, industrial, household or other chemical or compound. Exemplary pharmaceutical agents are disclosed in Table 1.

The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes complementary to the genes associated with hypersensitivity. The genes used may comprise at least two genes, at least 3, 4, 6, 7, 8, or 9 genes predetermined to be associated with hypersensitivity, and may also comprise at least 5, at least 10, at least

25, at least 50, at least 100, at least 250 or more genes determined to be associated with hypersensitivity.

Genes associated with hypersensitivity and used in this invention may, for example, comprise genes from a variety of different cell types, including, but not limited to, genes  
5 from multiple types of tissues, organs or systems or genes from a single type of tissue, organ or system. Exemplary organs and tissues include the liver, kidneys, heart, brain, thyroid, lung, pancreas, muscle, brain, testes, ovaries, spleen, stomach, intestines, colon, rectum, eyes, muscle, skin, and bone. Exemplary types of cells include liver cells such as, Kupfer cells, sinusoidal cells, ito cells, hepatocytes, bile duct epithelial cells, hepatic venule  
10 endothelial cells and sinusoidal epithelial cells.

A further embodiment encompasses the expression profile of the genes predetermined to be associated with hypersensitivity where expression of the genes is related to prevention or repair of toxic damage at the nucleotide, protein, macromolecule, organelle, cell, tissue, organ or system level.

15 In another embodiment, the gene expression profile may comprise a profile of protein expression levels, where the proteins are encoded by genes associated with hypersensitivity. The level of expression of the proteins may be directly related to the prevention or repair of toxic damage at the protein, nucleotide, macromolecule, organelle, cell, tissue, organ or system level. An additional embodiment includes protein expression  
20 profiles, where the proteins are encoded by genes associated with hypersensitivity, and the expression of the genes is, for example, associated with response to the presence of an agent, such as a toxic agent. Exemplary agents that can induce a characteristic profile of protein expression associated with hypersensitivity include those agents listed in Table 1.

The gene expression profile may be obtained from a sample from the subject, which  
25 sample may be from a cell or tissue sample and may comprise cells of different cell types. For gene expression, the sample may comprise, for example, white blood cells, skin, spinal

fluid or organ biopsy material. For protein expression analysis, the sample may comprise, for example, blood, tissue, urine, spinal fluid or serum.

In another embodiment, cells or tissues derived from an individual are used to establish primary cell cultures, for example fibroblasts, hepatocytes, and other examples known in the art. These primary cell cultures are then exposed to the agent. Co-cultures are also encompassed in the invention and are grown from two or more cell types that reflect, for example, the cell types involved in systemic toxicity. These co-cultures would then be exposed to the agent of interest.

In another embodiment, the gene expression profiles of samples from normal individuals, hypersensitive individuals or cell cultures are determined for individual agents using the methods herein described to determine drug-drug interactions. The gene expression profiles are compared to determine whether the multiple agents, for example two or more agents, elicit the same or similar gene expression profiles in the samples. The expression of the same or similar pattern(s) of toxic response genes for two or more compounds in either normal or hypersensitive individuals, is indicative that a drug-drug interaction, also described as a synergistic toxic effect, can be present if the agents are administered together, for example, during the same time period or in the same dose.

The genes used in the gene expression profile may include, but are not limited to, genes, and the proteins which they encode, which are associated with toxic outcomes affecting the pulmonary system, cardiovascular system, nervous system, digestive system, immune system, reproductive system, endocrine system, vision or skin. Exemplary types of toxicity include cardiotoxicity, blood toxicity, liver (hepatic) toxicity, kidney (renal) toxicity, neural toxicity, skin toxicity, immunotoxicity, and pulmonary toxicity. Exemplary genes associated with specific organ or system toxic outcomes are disclosed in Table 5.

The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, altered lipid

metabolism, altered thyroid function, organ hypertrophy, skin irritation, skin sensitization, tumor formation, dementia, inflammation, myelosuppression, peripheral neuropathy, necrosis, signal refractivity, spreading, transformation, retinopathy or optic atrophy.

5       The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the digestive system or the organs and tissues which comprise the digestive system, for example, the liver, kidneys, colon, bladder, pancreas, stomach, intestines, rectum, or gallbladder.

10      The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with exemplary toxic outcomes such as, but not limited to, proteinuria, glomerulitis, nephritis, renal damage, renal failure, liver weight change, cholestasis, pancreatitis, liver steatosis, hyperplasia, fatty liver, jaundice, hepatitis, mutagenesis, or altered bile flow.

15      The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the pulmonary system or the organs and tissues which comprise the pulmonary system, for example the lungs or trachea.

20      The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, lung fibrosis, pulmonary edema or lung airway reactivity.

25      The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the cardiovascular and circulatory systems or the organs, fluids and tissues which comprise the cardiovascular and circulatory systems, for example, the heart, spleen, arteries, blood vessels, blood or blood cells, including genes associated with toxic outcomes associated with bone marrow.

The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with exemplary toxic outcomes such as, but not limited to, tachycardia, arrhythmia, leukemia, neutropenia, hematological alteration, hypotension, hypertension or agranulocytosis.

5 The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the nervous system or the organs and tissues which comprise the nervous system, for example, the brain, spinal cord or nerves.

10 The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, neurodegeneration or neurotoxicity.

15 The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the immune system or the organs and tissues which comprise the immune system, for example, the thymus, lymph nodes or lymph glands.

The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, a change in thymic weight or immunosuppression.

20 The genes used in the gene expression profile may include, but are not limited to genes, and the proteins which they encode, which are associated with toxic outcomes affecting the reproductive system or the organs and tissues which comprise the reproductive system, for example the testes, ovaries, fallopian tubes or uterus.

25 The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with toxic outcomes such as, but not limited to, teratogenesis, loss of fertility, alteration in sperm count, alteration in testes weight or alteration in testosterone levels.

The genes used in the gene expression profile include those genes, and the proteins which they encode, associated with cellular manifestations of toxicity such as, but not limited to, apoptosis, cell adhesion, autophagocytosis, cell division, chemotaxis, cell cycle arrest, circadian rhythm, cytokine release, differentiation, de-differentiation, mitochondrial damage, migration, mutation, oncosis, recombination, senescence, peroxisome proliferation, polyploidy, signal refractivity, spreading, transformation or necrosis.

5 The genes involved, and the proteins which they encode, may also include those associated with a specific ethnic group, sex or age group.

10 The genes or proteins used in the expression profile may also include the genes, and the proteins or amino acids which they encode, which are selected from the genes disclosed in (or genes comprising sequences disclosed in) Table 3, Table 4, Table 5, Table 6, Table 8, Table 10 and Table 11.

15 In another embodiment, the method includes obtaining a gene expression profile of genes comprising different cell types, of the subject, determining if the gene expression profile of the subject comprises a pattern of gene expression associated with hypersensitivity to an agent, and withholding that agent from those subjects who are hypersensitive or altering the therapy and closely monitoring the subjects who are hypersensitive for toxic effects.

20 In another embodiment, a method of identifying a plurality of genes associated with hypersensitivity to an agent is provided, comprising comparing the gene expression profile of cells treated with an agent with the gene expression profile of cells not treated with the agent and identifying genes that have altered expression due to exposure to the agent in the treated cells. The cells may comprise, for example, a number of different cell types and each cell type may comprise a gene associated with hypersensitivity to the agent. The cells 25 may also comprise cells from of different cell types where all the cell types are derived from a single type of tissue, organ or system. The organs or tissues from which cell types

may be derived include, but are not limited to, the kidneys, liver, lungs, heart, brain, spleen, thyroid, bone, muscle, intestine, stomach, pancreas, testes, ovaries, colon or skin.

The invention also relates to a method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent by comparing the  
5 gene expression profile of one or more cell types, for example, at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100 or at least 250, of a subject known to be hypersensitive to the agent with the gene expression profile of the cell types in an individual known not to be hypersensitive to the agent and identifying genes from the two or more cell types which exhibit a pattern of differential gene expression associated with  
10 hypersensitivity to the agent.

In an alternative embodiment, the method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent comprises comparing the gene expression profile of one or more cell types, for example, at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100 or at least 250, of a subject known to  
15 be hypersensitive to the agent before treatment with the agent with the gene expression profile of the one or more cell types of the subject after treatment with the agent and identifying genes from the cell types having a pattern of differential gene expression associated with hypersensitivity to the agent.

In an alternative embodiment, the method of identifying proteins having a pattern of differential protein expression indicative of hypersensitivity to an agent comprises comparing the protein expression profile of one or more cell types of a subject known to be hypersensitive to the agent before treatment with the agent with the protein expression profile of the one or more cell types of the individual after treatment with the agent and identifying proteins from the cell types having a pattern of differential protein expression  
25 associated with hypersensitivity to the agent.

In another embodiment, there is provided an array for the identification of a gene expression profile indicative of a hypersensitivity to an agent which comprises gene probes,

for example, nucleic acid sequences which comprise a gene sequence associated with hypersensitivity to the agent, associated with the hypersensitivity to the agent. The genes are selected from the genes identified by methods disclosed herein or are selected from those genes disclosed in whole or in part in Table 3, Table 4, Table 5, and Tables 6, 8, 10 and 11. The array comprises for example, at least 5, at least 10, at least 25, at least 50, at least 100, at least 150, at least 250 different gene probes. Exemplary arrays include, for example, gene probes supported on glass slides or nylon membranes with fluorescent or radio labels, amplified fragment length polymorphism (AFLP) methods or Northern Blots.

The invention further encompasses a database of genes associated with hypersensitivity to an agent. The genes are those identified by methods disclosed herein or are selected from those genes disclosed in whole or in part in Table 3 and Table 4, Table 5 and Tables 6, 8, 10 and 11. The database of genes may comprise, for example, genes associated with altered lipid metabolism, cholestasis, immunosuppression, pancreatitis, agranulocytosis, tumor formation, teratogenesis, liver steatosis, apoptosis, cell adhesion, autophagocytosis, cell cycle arrest, circadian rhythm, cytokine release, differentiation, migration, oncosis, recombination, senescence, signal refractivity, spreading, transformation, peroxisome proliferation, necrosis, glomerulitis, nephritis, arrhythmia, hypotension, hypertension, leukemia, neutropenia renal damage, renal failure, pulmonary edema, neurotoxicity or retinopathy.

The invention further encompasses a method for identifying individuals who may be hypersensitive to the toxic side effects of drugs such as those listed in Table 1 or industrial compounds such as those listed in Table 2.

An additional embodiment includes an apparatus for identifying hypersensitivity in a subject comprising means for obtaining a gene expression profile of a number of genes associated with hypersensitivity of the subject suspected to be hypersensitive; and means for identifying in the gene expression profile of the subject a pattern of gene expression of

the genes associated with hypersensitivity, thereby to identify hypersensitivity in the subject.

Also provided are methods of determining hypersensitivity of an individual to an agent, such as a pharmaceutical drug, such as penicillin, by detecting a gene expression or protein expression profile of the individual, wherein the genes or proteins encoded therefrom are selected from genes listed in whole or in part in Tables 10 and 11. The pattern of expression may be detected in a cell, such as an immune cell, such as a leukocyte, e.g. a lymphocyte.

Also provided are devices for detection of gene expression profiles comprising nucleic acid sequences for detecting expression of the nucleic acids disclosed in the Tables, for example by hybridization. Such devices include, for example, immobilized nucleic acid arrays.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a graph illustrating gene expression changes associated with toxicity caused by streptozotocin.

Figure 2 is a graph illustrating co-induction of genes for hepatocyte growth factor receptor and glutathione transferase.

Figure 3 is a graph illustrating a portion of a gene expression profile from heart muscle tissue after exposure to the cardiotoxin, doxorubicin.

Figure 4 is a graph illustrating a portion of a gene expression profile from liver tissue after exposure to the peroxisome proliferation caused by WY 14,643.

Figure 5 is a graph illustrating a portion of a gene expression profile from liver tissue after exposure to the anti-neoplastic compound, carbamazepine.

Figure 6 is a chart illustrating the result of testing for penicillin hypersensitivity amongst a group of penicillin sensitive and penicillin refractive individuals by using a 180 gene penicillin array.

Figure 7 is a chart illustrating the result testing for penicillin hypersensitivity amongst a group of penicillin sensitive and penicillin refractive individuals by using a 20 gene penicillin array.

Figure 8 is a chart illustrating 20 discriminator genes analyzed for co-regulation.

5       Figure 9 is a graph illustrating the results of a Taqman® assay in a penicillin sensitive person.

Figure 10 is a graph illustrating the results of a Taqman® assay in a penicillin refractive person.

10

#### BRIEF DESCRIPTION OF THE TABLES

Table 1 is a list of pharmaceutical agents which potentially can cause greatly heightened toxic responses in some individuals.

15       Table 2 is a list of industrial agents which potentially can cause greatly heightened toxic responses in some individuals.

Table 3 is a list of genes, altered expression patterns of which can indicate and render an individual hypersensitive to drugs and chemical agents.

Table 4 is a list of genes, altered expression patterns of which can indicate and render an individual hypersensitive to drugs and chemical agents.

20       Table 5 is a list of genes associated with specific manifestations of organ or system toxicity.

Table 6 is a list of genes that can be associated with specific cellular manifestations of toxicity.

25       Table 7 lists compounds for which gene expression data in either human cells, rats or both has been generated.

Table 8 lists genes whose expression was measured when rats were exposed to the cardiotoxin doxorubicin.

Table 9 lists cell types in organs of toxicity.

Table 10 lists the characterization of genes which were isolated and sequenced from gel bands.

Table 11 lists the genes that are useful discriminator genes.

5

### DETAILED DESCRIPTION OF THE INVENTION

Provided are methods, compositions and apparatus for identifying hypersensitivity  
10 in an individual. In one embodiment, hypersensitivity in a subject is determined by obtaining from the subject a sample from which can be determined the gene expression profile of genes associated with hypersensitivity, and identifying in the gene expression profile the presence or absence of a pattern of gene expression of the genes associated with hypersensitivity, thereby to identify hypersensitivity in the individual.

15

#### General Techniques

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are within the skill of the art. Such techniques are explained fully in the literature, such as, *Molecular Cloning: A Laboratory Manual*, second edition (Sambrook *et al.*, 1989); *Oligonucleotide Synthesis* (M.J. Gait, ed., 1984); *Animal Cell Culture* (R.I. Freshney, ed., 1987); *Handbook of Experimental Immunology* (D.M. Weir & C.C. Blackwell, eds.); *Gene Transfer Vectors for Mammalian Cells* (J.M. Miller & M.P. Calos, eds., 1987); *Current Protocols in Molecular Biology* (F.M. Ausubel *et al.*, eds., 1987); *PCR: The Polymerase Chain Reaction*, (Mullis *et al.*, eds., 1994); *Current Protocols in Immunology* (J.E. Coligan *et al.*, eds., 1991); *The Immunoassay Handbook* (David Wild, ed., Stockton Press NY, 1994); *Antibodies: A*

*Laboratory Manual* (Harlow *et al.*, eds., 1987) and *Methods of Immunological Analysis* (R. Masseyeff, W.H. Albert, and N.A. Staines, eds., Weinheim: VCH Verlags gesellschaft mbH, 1993).

5      Definition of Terms

As used herein, the terms 'gene', 'polynucleotide', 'nucleotide' and 'nucleic acid' are interchangeable and refer to polynucleotide sequences, which for example, encode protein products and encompass mRNA, cDNA, single stranded DNA, double stranded DNA and fragments thereof.

- 10     The terms "protein", "polypeptide", and "peptide" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non-amino acids. It also may be modified naturally or by intervention; for example, disulfide bond formation, glycosylation, myristylation, acetylation, alkylation, phosphorylation or dephosphorylation.
- 15     Also included within the definition are polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids) as well as other modifications known in the art.

The terms 'stress gene', 'toxicity gene' and 'toxic response gene' as used herein are interchangeable. A toxic response gene can be defined as a gene whose message or protein level is altered by adverse stimuli. The specific set of genes that cells induce is dependent upon the type of damage or toxic threat caused by the agent and which organs are most threatened. In addition to the up-regulation of genes which respond to specific toxic threat, genes which encode functions not appropriate under conditions of toxic injury may be down-regulated.

- 25     As used herein, 'toxic outcome' refers to the microscopic or macroscopic symptoms, physiological, morphological or pathological changes which are observed as a result of exposure to an agent.

A 'toxic response' as used herein refers to a cellular, tissue, organ or system level response to exposure to an agent and includes, but is not limited to, the differential expression of genes and/or proteins encompassing both the up- and down-regulation of such genes; the up- or down-regulation of genes which encode proteins associated with the repair or regulation of cell damage; or the regulation of genes which respond to the presence of an agent.

A 'gene expression profile associated with hypersensitivity' as used herein refers to the pattern of relative levels of gene expression found to be associated with hypersensitivity. Gene expression profiles may be measured in a sample, such as samples comprising a variety of cell types and may, for example, comprise blood, urine, spinal fluid or serum.

A 'protein expression profile associated with hypersensitivity' is defined as the pattern of relative levels of protein expression where said proteins are encoded by genes determined to be associated with hypersensitivity. For each gene expression profile that is determined, a corresponding 'protein expression profile associated with hypersensitivity' may be determined.

The terms 'up-regulation' and 'induction' are used interchangeably herein and refer to the regulation of gene expression, specifically the turning on of a particular gene(s). Similarly, the terms 'down-regulation' and 'repression' are used interchangeably herein and refer to the suppression of expression of a particular gene(s).

An 'agent' to which an individual is hypersensitive is defined as any substance to which an individual may be hypersensitive and includes, but is not limited to, drugs, household chemicals, industrial chemicals and other chemicals and compounds to which individuals may be exposed.

'Hypersensitivity', as used herein, refers to the exaggerated micro- or macroscopic responses of cells, tissues, organs or systems to low or average doses of an agent. These responses may lead to observable symptoms such as dizziness or nausea and can also result

in toxic outcomes. Hypersensitivity often results in toxic side effects that are different, in either degree or kind, from the response of the majority of patients at the recommended dose. Hypersensitivity may be characterized by, but is not limited to, the differential expression of genes when compared to the response of a similar individual who is not hypersensitive to a given agent. Hypersensitive individuals do not have normal gene expression patterns of key toxicologically relevant genes either prior to, or after, exposure to an agent.

5           ‘Differential expression’ as used herein refers to the change in expression levels of genes, and/or proteins encoded by said genes, in cells, tissues, organs or systems upon exposure to an agent. As used herein, differential gene expression includes differential transcription and translation, as well as message stabilization. Differential gene expression encompasses both up- and down-regulation of gene expression.

10           The term ‘individual’ is used interchangeably with the term ‘subject’ and ‘patient’ and refers to a mammal, preferably the primate, more preferably the human.

15           The term ‘normal individual’ or ‘normal subject’ refers to individuals who exhibit the same or similar dose response curves to an agent as does the majority of the exposed population. Most drugs at high enough dosages will cause a toxic response, therefore a ‘normal toxic response’ refers to the toxic response elicited in an average or normal individual at high doses of an agent.

20           The term ‘sample’ as used herein refers to samples for testing or analysis. The samples may comprise cells or tissue samples and may be, for example, blood, urine or serum. Samples are characterized in a preferred embodiment by comprising at least two different genes and may also include genes from multiple cell types. Samples include, but are not limited to, those of eukaryotic, mammalian or human origin.

25           As used herein, “array” and “microarray” are interchangeable and refer to an arrangement of a collection of nucleotide sequences in a centralized location. Arrays can be on a solid substrate, such as a glass slide, or on a semi-solid substrate, such as

nitrocellulose membrane. The nucleotide sequences can be DNA, RNA, or any permutations thereof. The nucleotide sequences can also be partial sequences from a gene, primers, whole gene sequences, non-coding sequences, coding sequences, published sequences, known sequences, or novel sequences.

5 "Penicillin sensitive" refers to individuals who exhibit hypersensitivity to penicillin, for example, a higher than average immune response to penicillin. The immune response can be a hypersensitive response of any type, for example Type I, II, III, or IV. Hypersensitive reactions can include but are not limited to anaphylaxis, skin rash, and hives. Hypersensitive responses also include hypertoxicity.

10 "Penicillin refractive" or "penicillin insensitive" or "penicillin non-sensitive" as used herein refers to individuals who exhibit a normal or non-hypersensitive response to penicillin.

#### Isolating DNA/RNA from human PBL

15 Nucleotide sequences from human peripheral blood lymphocytes (PBL) are isolated using any number of commercially available kits i.e. from Qiagen, GenHunter, Promega, etc.

In one embodiment, total RNA is isolated from tissue samples using the following materials: Qiagen RNeasy midi kits, 2-mercaptoethanol, liquid N<sub>2</sub>, tissue homogenizer, dry  
20 ice. It is important to take precautions to minimize the risk of RNA degradation by RNases by wearing gloves at all times and to inhibit RNase activity in work areas and equipment by treating with an RNase inhibitor such as with "RNase Zap" (Ambion® Products, Austin, TX). Autoclaving tips and microfuge tubes does not necessarily eliminate RNase enzymes and its RNA degradation activities. Samples are kept on ice when specified . Protocol  
25 which can be used is based on Qiagen® RNeasy® midi kit. This total RNA isolation technique is used for RNA isolation from human PBL and can be modified readily by one of skill in the art to accommodate different amount of human PBLs. The human PBL is

preferably taken from circulating blood of a human donor. However, human PBL can also be obtained from lymph nodes, spleen, and other tissues into which human PBLs circulate.

If tissue containing human PBL is used, then the tissue needs to be microdissected. One way is to physically break the tissue by placing it on a double layer of aluminum foil which is then placed within a weigh boat containing a small amount of liquid nitrogen. The aluminum foil is folded around the tissue and then the tissue is struck by a small foil-wrapped hammer to administer mechanical stress forces.

To preserve integrity of the RNA, all tissues are kept on dry ice when other samples are being weighed. A buffer is added to the sample to aid in the homogenization process. An example of a buffer which can be used is RLT (Qiagen®) buffer. The tissue is homogenized using any type of commercially available homogenizer (i.e. IKA Ultra Turrax T25 homogenizer, Virtishear Cyclone 750W rotor/stator homogenizer (Virtis item # 278077, etc.) can be used with the 7 mm microfine sawtooth shaft and generator (195 mm long with a processing range of 0.25 ml to 20 ml, item # 372718). After homogenization, samples are stored on ice until all samples are homogenized. The homogenized tissue sample can then be spun to remove nuclei thus reducing DNA contamination. The supernatant of the lysate is then transferred to a clean container containing an equal volume of 70% EtOH in DEPC treated H<sub>2</sub>O and mixed. In the event that a stringy white material comes out of solution, it may then be removed. RNA is isolated by putting the supernatant through an RNeasy spin column, washed, and subsequently eluted.

In another embodiment, DNA or RNA is isolated from human PBLs obtained from a human donor. Generally, lymphocytes can be isolated from blood by separating the blood over a gradient, for example a sucrose gradient or Percoll™ or Ficoll™ gradient. Lymphocytes can be distinguished from non-lymphocyte contaminants by morphology, size and scatter by flow cytometry, or by cell surface markers such as CD2, CD3, CD4, or CD8. In general, lymphocytes which are cultured *in vitro* are non-adherent but in some instances, lymphocytes can be adherent or non-adherent depending on several factors, for

example, activation state of lymphocytes, receptors expressed on lymphocytes, and culture media contents. In some aspects, adherent cells are more problematic than non-adherent cells because of the necessity of an extra step to separate the adherent cells from the tissue culture container. However, a skilled artisan may solve this problem by treating the cells with cold PBS/EDTA solutions or an equivalent and use any number of commercially available kits, for example, from Qiagen or Ambion, to isolate the DNA or RNA from the cells. In one embodiment, total RNA of high quality and high purity can be isolated from cultured cells by using Qiagen RNeasy midi kits and 2-mercaptoethanol. This embodiment is exemplified in Example 2 *infra*. Precautions should be taken to minimize the risk of 5 RNA degradation by RNases by wearing gloves, treating work areas and equipment with an RNase inhibitor, for example RNase Zap (Ambion® Products, Austin, TX), and keeping samples on ice. Using a Qiagen® RNeasy® midi kit (50), this total RNA isolation technique can be used for any type of cell, including but not limited to human lymphocytes and cell derived from particular organs such as kidney, liver, lung, breast, neuronal cells, 10 skin, intestine, such as HepG2, Caco-2, MCF-7, Jurkat, Daudi, HL-60, MCL-5, SKBr-3, 15 SKOV-3, PC-3, WISH, and HeLa.

To practice this embodiment, cells are checked under the microscope to confirm viability. Cells are then dosed with an agent, which can be a drug, chemical, or pharmaceutical composition, when they reach confluence. In a preferred embodiment, the 20 cells are at least about 20% confluent, more preferably at least about 40% confluent, even more preferably at least about 60% confluent, and even more preferably about 80% confluent. It is preferable to avoid isolating RNA from flasks that have reached 100% confluence because the cells are no longer growing in log phase.

The adherent cells are washed and freshly prepared buffer, for example RLT buffer 25 (RLT buffer requires the addition of 10 µl beta mercaptoethanol for each 1.0 ml RLT), is added directly to the cell culture flask. The amount of RLT buffer differs with tissue container size. Enough RLT buffer is added to cover the surface area in which the adherent

cells are growing such that most of the adherent cells come into contact with the RLT buffer. In one embodiment, T-75 flasks receive about 3 ml RLT buffer and T-175 flasks receive about 5 ml RLT buffer. It is preferable to lightly agitate the flasks at this point. Cells exposed to RLT buffer become a gelatinous layer. The cells are allowed to sit for 4 minutes, then fluid is withdrawn and is placed into an RNase-free tube. An equivalent volume of 70% ethanol is added to each tube and vortexed to distribute evenly. In the event that a precipitate with a string-like appearance forms, it is acceptable to remove and discard this string-like precipitate. The fluid is applied to a spin column, centrifuged, and the column is washed and subsequently eluted for RNA samples. The elution can be precipitated using the LiCl precipitation protocol and resuspended in RNA storage buffer for future storage. The yield can be between 200-400 µg of total RNA from a T-75 flask with greater than 50% confluency.

The isolated DNA or RNA is amplified to generate a product which can be attached to a substrate. In a preferred embodiment, the substrate is a solid substrate (i.e. glass slide). The amplification process involves using primers which have a reactive group (i.e. amine group or derivative thereof) on one end of the primer, which is incorporated into the amplification product. One example of reactive primers that can be used is Amine Primers from Synthegen. The gene fragments which are attached to the glass slide can vary in length. The more nucleotides of a gene that are in the array, the tighter the binding and the greater the specificity in binding can occur. However, it is important to consider that longer fragments are more difficult to amplify and may contain point mutations or other errors associated with amplification. Therefore, the desired length of a gene or a fragment thereof that is to be included in the array should take into consideration the balance between a high specificity of binding obtained with a long (i.e. >1 kb) gene sequence with the high mutational rate associated with a longer fragment. The gene fragments attached to the glass slide are at least about 50 base pairs (bp) in length, more preferably at least about 100 bp in length, more preferably at least about 200 bp, even more preferably at least about 25

300 bp, even more preferably at least about 400 bp, even more preferably at least about 500 bp in length. In a preferred embodiment, the gene fragments are about 500 bp in length. The region of a gene that is used to attach to a solid substrate to generate an array can be any portion of the gene, coding, non-coding, 5' end, 3' end, etc. In a preferred embodiment, about 500 base pairs of the 3' end of canine gene related to toxicological responses are selected to be included in an array.

Several techniques are well-known to a skilled artisan for attaching a gene or a fragment thereof to a solid substrate such as a glass slide. One method is to attach an amine group, a derivative of an amine group, another group with a positive charge or another group which is reactive to one end of a primer that is used to amplify a gene or a gene fragment to be included in the array. Subsequent amplification of a PCR product will then incorporate this reactive group onto one end of the product. The amplified product is then contacted with a solid substrate, such as a glass slide, which is coated with an aldehyde or another reactive group which will form a covalent link with the reactive group that is on the amplified PCR product and become covalently attached to the glass slide.

Other methods using amino propyl silicane surface chemistry are disclosed by Corning Company at <<http://www.cmt.corning.com>> other methods for making microarrays which are readily accessible at <<http://cmgm.stanford.edu/pbrown/>>

In one embodiment of the invention, fluorescence-labeled single strand (or "first strand") cDNA probe is made from total or mRNA by first isolating RNA from control and treated cells, disclosed *supra*. This probe is hybridized to microarray slides spotted with DNA specific for toxicologically relevant genes. This is exemplified in Example 8-14. The materials needed to practice this embodiment are: total or messenger RNA, primer, Superscript II buffer, dithiothreitol (DTT), nucleotide mix, Cy3 or Cy5 dye, Superscript II (RT), ammonium acetate, 70% EtOH, PCR machine, and ice. The Cy<sup>TM</sup> dyes may be obtained from Amersham. The embodiment may also be practiced with equivalents of the

materials listed above, for example, SuperScript II may be replaced with an equivalent enzyme and Cy5 and Cy3 may be replaced with another fluorescent dye.

In one embodiment, a discrete amount of RNA, for example 20 $\mu$ g of total RNA or 2 $\mu$ g of mRNA, is used to generate cDNA. In a preferred embodiment, the volume is no more than 14  $\mu$ l. If RNA is too dilute, the samples are concentrated to a volume of less than 14  $\mu$ l in a centrifuge with vacuum (i.e. Speedvac) without heat. The Speedvac should be capable of generating a vacuum of 0 Milli-Torr so that samples can freeze dry under these conditions. It is preferable for the tubes containing RNA to be kept on ice to avoid RNA degradation until the next step is ready to proceed. Following standard techniques well-known in the art, cDNA samples are amplified from RNA templates. A mixture of fluorescent dyes is made for labeling the cDNA samples. A variety of dyes can be used. In one embodiment, Cy3 dye, which is pink-red, and Cy5 dye, which is blue, are used. The Cy dyes are light sensitive, therefore, any solutions or samples containing Cy-dyes should be kept out of light, i.e. cover with foil. Example 9-12 discloses preferred mixtures and methods of using Cy3 and Cy5 dyes for labeling cDNA samples and purification steps therewith.

In an embodiment wherein the sequences of toxicologically relevant genes are not known and canine cells are divided into two groups, untreated and treated, to identify toxicologically relevant genes as disclosed *infra*, Cy3 dye mixture is incubated with the cDNA of each treated sample and Cy5 dye mixture is incubated with the cDNA of each control sample. Following the methods disclosed in Example 9, a visible pellet can be seen which is pink/red for cDNA incubated with Cy3 and blue for cDNA incubated with Cy5. It is recommended that the tubes are centrifuged at a fixed position so the pellet will be at a known area in the tube. In some rare instances, the cDNA sample (or cDNA probe) is seen spread on one side of the tube instead of a tight pellet. If the pellet is white (no pink/red or blue), it is likely that the reaction has not occurred to maximal efficiency.

Purification of fluorescent probes

Purification of fluorescence-labeled first strand cDNA probes can be achieved in one embodiment using the following materials: Millipore MAHV N45 96 well plate, v-bottom 96 well plate (Costar), Wizard DNA binding Resin, wide orifice pipette tips for 200 to 300  $\mu$ l volumes, isopropanol, and nanopure water. It will be evident to a skilled artisan that equivalent products may be substituted in other embodiments, i.e. other types of tissue culture plates, binding resin from other commercially available sources, for example Qiagen. Plate alignment during centrifugation is important since misaligned plates can lead to sample cross contamination and/or sample loss. In one embodiment, probes are purified by binding to a resin. The binding resin can be obtained by itself or from a kit provided by any number of commercial sources, i.e. Qiagen, Promega, etc.

Fluorescence Readings of cDNA Probe

Incorporation of fluorescence into cDNA probes can be achieved by using a number of methods. In one embodiment, the following material is used: 384 well, 100  $\mu$ l assay plate (Falcon Microtest cat#35-3980) and Wallac Victor 1420 Multilabel counter (or equivalent). Prior to use as a cDNA probe in hybridization, cDNA probes are purified and concentrated as exemplified in Example 10.

It is preferable that a consistent amount of cDNA is pipeted into the plate wells because readings can vary with volume. Controls or identical samples can be pooled at this step, if required or desired. The Cy-3 and Cy-5 fluorescence are analyzed using a fluorimeter, luminometer, flow cytometer, or any equivalent device which can detect different fluorescent dyes at different wavelengths. In a preferred embodiment, the Wallac 1420 workstation programmed for reading Cy3-Cy-5 is used. A typical range for Cy-3 (20 $\mu$ g) is 250-700,000 fluorescence units. A typical range for Cy-5 (20 $\mu$ g) is 100-250,000 fluorescence units. Preferred settings for the Wallac 1420 fluorescence analyzer are as follows:

Cy3

CW lamp energy = 30445  
Lamp filter = P550 slot B3  
5 Emission filter= D572 dysprosium slot A4  
Emission aperture = normal  
Count time = 0.1 s

Cy5

10 CW lamp energy = 30445  
Lamp filter = D642 samarium slot B7  
Emission filter= D670 slot A8  
Emission aperture = normal  
Count time = 0.1 s

15

After detection of the cDNA probes, it is important to concentrate the cDNA probes so that they can be resuspended in hybridization buffer at an appropriate volume for hybridizing to the array. Internal normalization is achieved by taking into consideration the ratio of Cy5 fluorescence to Cy3 fluorescence in the treated and untreated canine cell groups,  
20 respectively.

Microarray Hybridization

Hybridization of labeled cDNA probes to single stranded, covalently bound DNA target genes on glass slide microarrays can be accomplished by a variety of methods. In 25 one embodiment, exemplified in Example 7, the following material are used: formamide, SSC, SDS, 2 µm syringe filter, salmon sperm DNA, hybridization chambers, incubator, coverslips, parafilm, and heat blocks. It is preferable that the array is completely covered to ensure proper hybridization. Hybridization buffer is prepared with consideration towards stringency. Stringency can be varied by increasing or decreasing the amount of 30 SSC and detergent (i.e. SDS, Triton, etc.). Stringency can also be varied by the temperature at which the hybridization occurs. A higher temperature tends towards high stringency conditions. A skilled artisan can determine, in a stepwise fashion, the stringency of the hybridization buffer desired. Clean slides and coverslips are desirable and can be

obtained using N<sub>2</sub> stream. Hybridization buffer is added to dried probe and mixed in the dark at room temperature and then brought to a higher temperature in a heat block. Each probe can remain in a heat block until it is ready for hybridization. The probe is applied to a slide or to a coverslip and then covered with slide. It is highly preferable to avoid the material at the bottom of the tube and to avoid generating air bubbles. This may mean leaving some residual volume in the pipette tip. Slides are then placed in a hybridization chamber, wrapped to prevent the liquids from desiccating. One problem that can occur with overly dried slides is increased fluorescence on the edge of the spot containing the target gene fragment to which the labeled cDNA probe binds. In an alternative, the hybridization chamber can have a built-in humidity gauge to avoid desiccation of the slides.

In a preferred embodiment, the slides are placed in a 42°C humidity chamber in a 42°C incubator for 18 to 24 hours. It is preferable to avoid probes or slides sitting at room temperature for long periods.

15 Post-Hybridization Washing

To obtain single stranded cDNA probes on the array, all non-specifically bound cDNA probe should be removed from the array. In one embodiment, removal of all non-specifically bound cDNA probe can be accomplished by washing the array using the following materials: slide holder, glass washing dish, SSC, SDS, and nanopure water.

20 Equivalents of SSC and SDS may also be used as substitutes. It is highly preferable that great caution be used with the standard wash conditions since deviations can affect data significantly.

In one embodiment, glass buffer chambers and glass slide holders are filled with heated SSC buffer with sufficient volume to submerge the microarrays. It is important to exercise caution in heating of the SSC buffer since a high temperature may strip off the probes, preferably the temperature is at most about 60°C, more preferably at most about 50°C, even more preferably at most about 40°C, and even more preferably at most about

35°C. A skilled artisan can vary the concentration of SSC in the buffer according to the stringency desired. The slides are placed in buffer which may contain SSC and/or detergent (i.e. SDS, Triton, etc.) and the coverslips are dislodged and fall off the slide within several minutes of submersion. In the event that the coverslips do not fall off within 5 several minutes of submersion, very gentle agitation may be administered to the chamber in which the wash is being conducted to dislodge the coverslips. The slides with the hybridized probes are subjected to several rounds of washes with different conditions. In one embodiment, a detergent (i.e. SDS) is added to the wash buffer in different concentrations and the slides are washed in this buffer before a final wash in nanopure 10 water. The slides are dried in a manner that will minimize background signal of the array. A preferred method of drying is to use a folded paper towel underneath the slide and a gently dabbing motion on the slide with a tissue. It is important that the slides do not air dry since this will lead to increased background.

15 Gene Expression Profiles

The pattern of gene expression characteristic of hypersensitivity is predetermined, and is, for example, provided in a database. By comparing the gene expression profile of the subject with the predetermined pattern of gene expression of multiple genes characteristic of hypersensitivity, the hypersensitivity of the subject can be conveniently 20 and rapidly determined. Advantageously, the invention provides a large number of predetermined gene expression patterns of genes associated with hypersensitivity, for example in a database, so that a large number of genes can be rapidly analyzed and compared in the subject. Analysis of information about expression of a wide spectrum of genes associated with hypersensitivity facilitates the rapid determination of hypersensitivity 25 of a subject to an agent, or multiple agents.

For example, the differential gene expression profile associated with a given agent can be determined for a given agent using, for instance, eukaryotic or mammalian cells or

cell lines or animal models and exposing a population of the eukaryotic or mammalian cells or cell lines or animal models to an agent and comparing their gene expression to the same type of eukaryotic or mammalian cells or cell lines or animal models from an untreated population to determine the gene expression profile associated with hypersensitivity.

5       Hypersensitivity to an agent, for example, a pharmaceutical drug or household, industrial or other chemical, can be rapidly determined with samples from an individual or group of individuals by treating the sample(s) with an agent and comparing the gene expression profile with the gene expression profile associated with hypersensitivity determined previously for a particular agent and, for instance, stored in a database and  
10      accessed and compared with associated software.

Table 1 lists approximately 200 drugs sold in the U.S. and Europe. There are individuals who are hypersensitive to the toxic side effects of each of these drugs. Table 2 lists at least 100 major industrial chemicals for which there is documented evidence of toxicity due to occupational exposure. For each of these chemicals there are individuals  
15      whose toxic response is heightened compared to the majority of the population.

In a preferred embodiment, multiple genes are analyzed. Preferably, the number of genes, associated with hypersensitivity, whose expression levels are determined and which comprise the gene expression profile is large; for example, one or more, at least 2, at least 3, at least 4, at least 5, at least 10, at least 50, at least 100, or at least 250. The present  
20      invention also encompasses gene expression profiles where the number of genes is greater than 400, 500, 600 or more.

In another embodiment, the genes, whose expression levels comprise the gene expression profile, are drawn from a variety of cell types.

For example, the genes, whose expression levels comprise the gene expression  
25      profile, are drawn from cells of a number of different tissues or organs.

In another embodiment, cells or tissues derived from an individual are used to establish primary cell cultures, for example fibroblasts, hepatocytes, and other examples

known in the art. These primary cell cultures are then exposed to the agent. Cell cultures established from the appropriate tissues of hypersensitive individuals are more sensitive to the toxic effects of the agent than cultures established from normal individuals. This hypersensitivity is reflected in the gene expression patterns elicited from the cell cultures.

5        In another embodiment, cells or tissues derived from an individual are used to establish primary cell cultures, for example fibroblasts, hepatocytes, and other examples known in the art. Co-cultures would be grown from two or more cell types that reflect the cell types involved in systemic toxicity. These co-cultures are then exposed to the agent of interest. Cell co-cultures established from the appropriate tissues of hypersensitive  
10      individuals are more sensitive to the toxic effects of the compound than co-cultures established from normal individuals. This hypersensitivity is reflected in the gene expression patterns elicited from the cell co-cultures.

15      In another embodiment, the gene expression profile consisting of the expression levels of multiple genes includes genes drawn from a single cell, tissue or organ type, and the profile is examined to determine the association of the gene expression profile with hypersensitivity.

20      In addition to the determination of absolute levels of expression for the genes in the gene expression profile associated with hypersensitivity, the relative expression levels of two or more genes in the gene expression profile associated with hypersensitivity can be determined and can be relevant to a determination of hypersensitivity. Hypersensitive individuals will have profiles of expression of relevant toxicity genes that are distinct from individuals who are not hypersensitive.

25      In another embodiment, gene expression profiles from normal individuals, hypersensitive individuals or cell cultures are established for individual agents to determine possible toxic drug-drug interactions when patients (normal or hypersensitive individuals) are treated with multiple drugs. There are hundreds of combinations of compounds that are more toxic when taken together than when taken singly. Usually these toxic drug-drug

interactions are discovered as clinical manifestations once the drugs reach market.

Examples of compounds that cause severe toxicity when taken together include cyclosporin A and trimethoprim, Walworth *et al.* (*Lancet*) 1:336(1983); and Clonidine and Tricyclic antidepressants such as Amoxapine. Briant *et al.* (*Br J Pharmacol*) 46:563(1972). The

5 expression of the same pattern of toxic response genes for two or more compounds in either normal or hypersensitive individuals, indicates that the two or more compounds, taken together, will often show a synergistic toxic effect. Gene expression profiles for each compound, determined *in vitro* or *in vivo*, allows prediction of the severe toxicity if the two compounds were taken together.

10 In another embodiment, the gene expression profile of genes associated with certain disease states is analyzed. Normal individuals can become temporarily hypersensitive to the toxicity of certain drugs because of disease states. Hypersensitivity is present in normal individuals when toxic defense mechanisms are temporarily compromised. For example, an individual who suffers from AIDS-induced immunosuppression will be hypersensitive  
15 to the toxic effects of immunosuppressive compounds such as cyclosporin A. An individual suffering from pulmonary edema due to viral infection will be temporarily hypersensitive to compounds such as bleomycin which elicit pulmonary edema as a toxic side-effect.

20 In another embodiment, the method includes obtaining a protein expression profile of a number of proteins encoded by genes of the subject, determining if the protein expression profile of the subject comprises a pattern of protein expression associated with hypersensitivity to an agent, and withholding the agent from those individuals or altering the therapy or dosage and closely monitoring the individual for toxic effects.

25 In addition, a method of identifying a number of genes associated with hypersensitivity to an agent is provided comprising comparing the protein expression profile, where the proteins are encoded by the genes identified as associated with hypersensitivity to the agent, of cells treated with the agent with the protein expression

profile of cells not treated with the agent and determining proteins that have altered expression due to the exposure to the agent in the treated cells. The cells may comprise, for example, a variety of different cell types and each cell type may comprise a gene associated with hypersensitivity to the agent, and the protein encoded by gene.

5 An additional embodiment includes a method of identifying a number of genes associated with hypersensitivity to an agent which comprises comparing the protein expression profile, where the proteins are encoded by the genes identified as associated with hypersensitivity to the agent, of cells treated with the agent with the protein expression profile of the same type of cells from the same subject not treated with the agent and  
10 determining proteins that have altered expression due to exposure to said agent in the treated cells. The cells may comprise, for example, a variety of different cell types and each cell type may comprise a gene associated with hypersensitivity to the agent, and the protein encoded by the gene.

In a further embodiment, the gene expression profile of multiple genes associated  
15 with cellular response to toxic agents are analyzed to determine the association with hypersensitivity of the genes in the profile.

Using the methods, compositions and devices disclosed herein, rapid, accurate and inexpensive tests of an individual can be conducted in order to confirm whether the individual is hypersensitive to an agent. For example, an individual can be screened for  
20 hypersensitivity to a drug before the drug is administered. Such screenings avoid incidents of hypersensitivity in individuals to whom a drug might otherwise be administered. Alternately, the drug can be given in lower doses to hypersensitive individuals and/or those individuals considered at risk may be closely monitored for adverse reactions to the agent. Avoiding exposing hypersensitive individuals to any given drug or compound, or to a  
25 higher than necessary dose or level of the drug or compound, provides cost savings to manufacturers who may produce the drug or compound with an assurance that hypersensitivity reactions will be avoided. Those who are not hypersensitive may safely

receive the drug or compound and receive its benefits, while those who are hypersensitive may safely avoid the drug or be prescribed a different drug or in the case where the toxicity is due to exaggerated pharmacological effects, a smaller, but just as effective dose.

The invention also encompasses using the methods, composition and devices disclosed herein for rapid, accurate and inexpensive tests that can be used, for instance, to determine the causative agent in an individual exhibiting symptoms consistent with or indicative of a toxic response or hypersensitivity to various agents. By ascertaining the gene profile of a number of genes associated with particular cells, tissues, organs or systems, the agent eliciting the toxic response or hypersensitivity may be determined and thereon avoided. In one embodiment, gene expression analysis might be used to determine the nature of the toxic insult and thus provide treatment. For example, analysis of expression of tox-response genes might aid in the effective diagnosis and treatment of an unconscious child suspected of having been inappropriately exposed to a drug or chemical agent. Gene expression patterns could be useful in determining if the unconscious state were the result of exposure to a soporific agent or one that inhibited mitochondrial function, the treatments of which would be quite distinct.

Exemplary genes associated with hypersensitivity whose expression may be screened in order to determine hypersensitivity are provided in whole or in part in Tables 3, 4, 5, 6, 8, 10 and 11. Also provided herein are methods of identifying genes associated with hypersensitivity.

#### Genes

Tables 3, 4, 5, 6, 8, 10 and 11 provide a list of exemplary genes from which genes associated with hypersensitivity to a particular agent may be selected. Genes selected from Table 3 and Table 4 are responsive to toxic stimuli and important to the defense or repair of toxic damage. Individuals with significantly altered expression levels of two or more of the genes in Tables 3, 4, 5, 6, 8, 10 and 11 can also show different toxic responses from normal

individuals. For a given agent, the expression profile of two or more genes, for example, selected from Tables 3, 4, 5, 6, 8, 10 and 11 can be obtained from a cell, tissue or organ and, a pattern of gene expression predetermined to be associated with hypersensitivity can be established.

5       Genes such as those selected from Tables 3 and 4 are evaluated for differential gene expression, for example in the major toxic target organs in humans and/or rats and mice. Examples of genes in which differential expression is indicative of toxicity or hypersensitivity in specific organs or systems such as liver (hepatic), kidney (renal), lung (pulmonary), central nervous system (neural), heart (cardio) and immune system are shown  
10      in Table 5.

As an example, Figure 1 shows the pattern of gene expression of approximately 250 genes in the liver when the subject received a relatively high dose of streptozotocin. Samples, including for instance, blood, urine, serum or tissue, from individuals known to be hypersensitive to streptozotocin can be obtained after the subject is treated with  
15      streptozotocin. Alternately, for example, samples may be from untreated individuals known to be hypersensitive to streptozotocin and the samples may then be treated *in vitro* with streptozotocin. The samples are then examined to identify genes associated with hypersensitivity. This may show, for example, highly exaggerated expression of toxic response genes and/or patterns of induction or repression of genes in treated individuals or  
20      upon *in vitro* treatment of the sample with streptozotocin compared to individuals who are not hypersensitive or sample which is not treated with streptozotocin. As streptozotocin is an example of a bulky alkylating agent, individuals who are hypersensitive to streptozotocin may be tested for hypersensitivity to compounds with similar toxic properties, such as bulky alkylating agents, such as merbarone and carmustine.

25      Genes whose levels of expression change in response to toxic stimuli may be evaluated. Examples of genes with expression changes in response to toxic stimuli are listed in Tables 3 and 4. The genes in Table 3 and Table 4 have been shown to be induced

in either cell lines, primary cells, tissues or tissue slices, from human or animal origin. For example, the GADD 153 gene has been shown to be induced in many human cell lines upon exposure to radiation. The environmentally important compound trichloroethylene was recently demonstrated to cause induction of several genes, including c-Myc and c-Jun in mice exposed to low toxic levels for 24 hr. Tao et al.(J Biochem Mol Toxicol) 13(5): 231-7 (1999). In primates, closely related to humans, hyperoxia causes increased expression of the genes encoding thioredoxin and thioredoxin reductase gene expression in lungs. Das et al., (Chest) 116(1 Suppl): 101S (1999).

Many of the genes in Tables 3 and 4 are known to be involved in the prevention or repair of damage to DNA, cells or tissue in response to toxic agents (several examples are provided by the following references: Kegelmeyer et al. (Mol. Carcinog.) 20(3): 288-97 (1997); Koerber et al. (Mol. Reprod. Dev.) 49(4): 394-9 (1998); Kuhn (Nutr. Rev.) 56:11-9, discussion 54-75 (1998); Lu et al. (Mol. Carcinog.) 20(2): 204-15 (1997); Muhlenkamp et al. (Toxicol. Appl. Pharmacol.) 148(1):101-8 (1998); Melhus et al. (Biochem. Mol. Biol. Int.) 43(5):1145-50 (1997); Pentecost (Steroid Biochem. Mol. Biol.) 64(1-2):25-33 (1998); Quattrochi et al. (Arch. Biochem. Biophys.) 349(2):251-60 (1998); Rout et al. (Cell Calcium) 22(6): 463-74 (1997); Sadekova. et al (Int. J. Radiat. Biol.) 72(6): 653-60 (1997); Yuan et al. (J. Biol. Chem.) 273(7):3799-802 (1998); Zhao et al. (Oncogene) 16 (3):409-15 (1998).

Table 6 shows a set of genes associated with specific types of cellular toxicity. Studies of single gene expression have shown over- or under- expression of certain of these genes, to affect the sensitivity of the cell or organism to toxic stimuli and are described in the art. Advantageously, the expression levels of all of these genes can be measured simultaneously. Individuals hypersensitive to an agent can be identified by measuring the expression patterns of the toxicity genes specific to that agent. Tables 3, 4, 5 and 6 are non-limiting examples of such toxicity genes.

Agents

Many compounds are toxic at a high enough concentration. For example, while most individuals might experience extreme tachycardia after receiving a very high dose – 20 times normal – of a drug, they experience no such effects at recommended doses. The 5 hypersensitive individual would experience extreme tachycardia at the recommended dose or at a lower than normal dose. A hypersensitive individual might also experience a qualitatively distinct toxic response to a compound, not just the same response that a normal individual would experience at high doses. For example, the hypersensitive patient might experience extreme dizziness, a side effect not reported by individuals even at high 10 doses.

Agents to which individuals may be hypersensitive, and for which hypersensitivity can be determined, may include, for example, drugs, industrial chemicals, household or other chemicals, including those in the workplace. Examples of drugs and industrial chemicals for which a sub-population is hypersensitive are listed in Tables 1 and 2.

15 As a further example, individuals who are employed in manufacturing or other environments which expose them to a variety of agents may be screened for agents to which they might come into contact. Individuals, or for example, a subset of workers, who are hypersensitive to the agents can then be identified. Hypersensitivity to other agents also may also be determined, such agents including, but not limited to biological agents 20 such as naturally occurring organic compounds, including proteins, saccharides and lipids.

Exemplary pharmaceutical agents include, for example, tienilic acid, halothane, dihydrazine, diclofenac, fialuridine, carbamazepine, Trovan<sup>TM</sup> (trovafloxacin), Seldane<sup>TM</sup> (terfenadine), hismanol, dihydrolazine, warfarin, phenytoin, omeprazole, diazepam, haloperidol, perphenazine, perhexiline, phenformin, tolbutamide, penicillin, clozapine, 25 aminopurine, quinidine and remoxipide. Table 1 lists additional agents for which there are individuals who demonstrate hypersensitivity.

Examples of other chemicals include industrial chemicals, such as paint, volatile organic compounds (VOCs), solvents, adhesives, pesticides, herbicides, perfumes, aerosols, cleaning compounds and synthetic polymers such as textiles.

5

### Identification of Genes

Genes initially suspected of being associated with hypersensitivity and hence potentially useful in the present invention are identified, for example, by conducting extensive literature searches; investigating known biochemical pathways with toxicological relevance; and measuring gene expression from toxin-exposed animals, humans or cell lines. Hypersensitivity to an agent, such as a drug, may also be determined based on the ability to identify the underlying molecular basis for the toxicity of specific drugs. Hypersensitivity can also be determined by examining the gene expression of hypersensitive and normal individuals.

In one embodiment, methods are provided wherein literature reports on the expression levels of single genes in response to a single agent are collected, for example, in a database, and then analyzed to establish patterns of expression that can be correlated to hypersensitivity. Advantageously, large amounts of data can be collected and analyzed, for example by software means. For example, Matrix Express<sup>TM</sup>, and Chem Profiler<sup>TM</sup> (Phase-1 Molecular Toxicology, Santa Fe, NM) accommodate capture and analysis of gene expression profiles. For example, it allows identification of induced genes from the total set of genes measured using a number of criteria; for example, statistical significance, two-fold, and 1.5 X the standard deviation. The software also allows the search of other profiles and determines the commonality between subsets, ranking profiles by several measures of similarity, for example, using all or a subset of the genes.

Experiments include both *in vivo* and *in vitro* responses to agents, for example, the exposure of eukaryotic, mammalian or human cells, and animals to agents listed in Table 7.

One ultimate benefit of this exercise is to reduce the need for animal testing. Each agent is tested at several concentrations and time points.

The toxicology of an agent is evaluated by measuring toxic insult by detecting observable changes in organ or system appearance and/or function, at the micro- or macroscopic levels. For example, a drug may cause changes in fatty acid metabolism in liver hepatocytes. This in turn causes observable changes in liver appearance, such as a specific toxicological outcome referred to as fatty liver. In order for cells, and thus tissues and organs, to undergo observable morphological changes due to toxic insult, they generally express a subset of genes differently than untreated cells. Thus, manifestations of toxic injury frequently require differential gene expression. Such genes that are differentially expressed in response to toxic injury are evaluated for use as genes associated with hypersensitivity in accordance with the present invention.

Thus, the expression of genes that are differentially expressed in total across cell, organ and tissue types in humans, in particular in response to toxic insult, may be evaluated to determine which genes have expression that is linked to hypersensitivity in an individual. Individuals who do not properly express the appropriate toxicity response genes for a specific compound will be hypersensitive to the toxic effects of that compound.

Organs are composed of tissues, which in turn are composed of various cell types. There is a core set of genes whose products are involved in functions essential to all cells, and whose expression is shared by most human cell types. In addition to these common core genes, each cell type expresses a set of genes that is unique to that cell type. When animals, including humans, are exposed to chemicals that cause damage to one or more organs, cells that comprise those organs attempt to mitigate or repair that damage by turning on genes that encode toxic-damage defense or repair proteins. The specific set of genes that cells induce is dependent upon the type of damage or toxic threat caused by the compound and upon which organs are most threatened. In addition to the genes that are induced to deal with the specific toxic threat, there may be genes which encode functions

that are not needed nor appropriate under conditions of toxic injury. Therefore, both the up- and down-regulation of genes can be measured in order to understand the molecular response to that compound, and the linkage of gene expression to hypersensitivity. The pattern of differential gene expression within the toxic target organs can be limited to a 5 relatively small number of genes, and may be very specific to both the organ being threatened and the type of damage. Such genes may be analyzed to determine which genes are responsible for hypersensitivity, for example, within a certain organ. Such genes may be analyzed to identify subsets of genes that are associated with hypersensitivity to certain agents.

10 The measurement of gene expression patterns is useful because many factors can affect the level of transcripts of toxicity genes, including mutations in the regulatory regions of genes, mutation in transcription factor that control the gene(s) of interest, and gene duplications and deletions. Examples of genes whose expression may be screened for association with hypersensitivity to certain agents are further discussed herein.

15 Genes associated with changes in expression levels due to adverse stimuli or toxic insult include, for example, genes which respond to the presence of a compound, and genes which respond to damage caused by a compound at, for example, the protein, nucleotide, macromolecular, membrane, cell, tissue, organ or system level. For example, certain proteins either prevent or repair toxic cellular injury. Individuals who do not express the 20 appropriate gene profile will suffer greater damage from toxic compounds through a lack of repair enzymes.

25 Toxic responses can be measured by pathological changes, for example, at the protein, nucleotide, cell, tissue, organ or system level. These pathological changes can be associated with differential gene expression of at least two genes. In addition, and the correspondence between the pathological change and the differential gene expression can be established. At the concentration where pathological outcomes are observable, gene expression changes are specific and causally related to the outcome. For example,

compounds that cause peroxisome proliferation as observed in the electron microscope, such as WY 14,643 (Sigma Chemicals; St. Louis, MO), a common toxicological compound known in the art, turn on genes causally related to peroxisome proliferation (See Figure 4). Compounds that cause DNA damage as manifested by increased mutations and cell-cycle disruption turn on genes required to alter the cell cycle and repair the damage (See Figure 5 below). Furthermore, since most drugs elicit pleiotropic effects, and are metabolized differently, there is a specific gene expression pattern for each compound, even though there may be a sub-pattern with all compounds that, for example, alkylate DNA at the O-4 position of thymine.

10       Genes associated with hypersensitivity also may be identified by examination of the gene expression profile of hypersensitive individuals differing from normal gene expression patterns of the genes associated with differential gene expression either before or after exposure to the particular drug in question.

15       Genes which may be identified and tested for their association with hypersensitivity to a certain agent include a variety of genes known in the art that are induced in mammalian or eukaryotic cells or cell lines exposed to high concentrations of chemicals. Genes associated with toxicological response that can be identified for predicting different types of hypersensitivity to different agents include, for example, those genes described in: Cattell (Semin. Nephro.) 19(3):277-87 (1999); Schnabel, M. et al. (Int. J. Mol. Med.) 1(3):593-5 (1998); Cruse et al. (Carcinogenesis) 20(5) 817-824 (1999); Fogg, S. et al. (Am. J. Respir. Cell Mol. Biol.) 20(4):797-804 (1999); Aoki et al. (FEBS Lett.) 333:114-118 (1993); Feuerstein et al. (Can. J. Physiol. Pharmacol.) 75(6):731-4 (1997); Rodrigo et al. (Scand. J. Gastroenterol.) 34(3):303-307 (1999); Schmidt et al. (Biochem. Biophys. Res. Commun.) 242: 529-533 (1996); Rockett et al. (Eur. J. Drug Metab. Pharmacokinet.) 22: 239-233 (1997); Rudat et al. (Int. J. Radiol. Bio.) 73: 325-330 (1998); Buters et al. (Proc. Natl Acad. Sci USA) 96(5): 1977-1982 (1999); Wang et al. (Cardiovasc. Res.) 35

:414-421 (1997); Pang et al. (*Ann. Hum. Genet.*) 62(3): 271-4 (1998); and Herrlich, et al. (*Biol. Chem.*) 378(11) :1217-29 (1997).

Many toxic response genes are induced to higher levels of expression only when needed. An individual can show a defective or hypersensitive response if a crucial protein is defective or is not produced in sufficient abundance when needed. Thus individuals who do not synthesize sufficient amounts of key proteins or produce defective proteins required to minimize the toxic damage from a given agent will suffer from greater toxic injury.

Altered levels of the gene products of the genes listed in Table 3, Table 4, Table 5 and Table 6 are likely to render the cell or organism hypersensitive to toxic stimuli, and there is great variability among the population in basal and induced levels of these genes. There have been many studies of some of these individual genes in the literature, some of which are discussed below. For example, a mouse knock-out mutant for the DNA repair gene PARP was shown to be hypersensitive to the toxicity and genetic damage caused by gamma-irradiation and MNU. Trucco C. et al. (*Mol Cell Biochem*) 193(1-2): 53-60 (1999). Humans with low basal or induced expression of the PARP gene will be hypersensitive to gamma-irradiation, MNU and all radiomimetic agents.

In another example, it was recently shown that DNA repair methyltransferase (Mgmt) knockout mice are hypersensitive to the toxic effects of several chemotherapeutic alkylating agents. Glassner et al. (*Mutagenesis*) 14(3): 339-47 (1999). Individuals with decreased expression of the Mgmt gene will be hypersensitive to the same compounds.

In another example, a ‘temporary’ knock-out of the cyclophilin-A gene in mice was made by injecting an anti-sense RNA against the cyclophilin A gene in rat neonatal cardiomyocytes. The expression level of the cyclophilin A gene was reduced by 93% and animals treated were hypersensitive to the toxic effects of t-butylhydroperoxide. Doyle et al. (*Biochem. J.*) 341( 1):127-32 (1999). Humans who show depressed levels of cyclophilin A gene expression are expected to be hypersensitive to the toxic effects of t-butylhydroperoxide and other compounds that form active oxygen radicals.

5 Polymorphisms occur in the human population for the gene encoding serum paraoxonase (PON1). The PON1 gene product plays a major role in the detoxification of organophosphate (OP) compounds. One polymorphism (Arg192 isoform) hydrolyzes diazoxon, soman and sarin slowly. Costa et al. (Chem. Biol. Interact) 119-120: 429-38  
5 (1999).

10 Genes associated with hypersensitivity can be selected from those in Table 3, which are induced by toxic damage and have important physiological roles in responding to toxic stimuli. For example, Rettie et al. (Epilepsy Res.) 35(3):253 (1999) showed that humans carrying a polymorphism that decreases expression of the CYP2C9 gene are very sensitive to compounds such as phenytoin and (S)-warfarin. The data demonstrate that the  
15 CYP2C9\*3 polymorphism gene product retains only 4-6% of the metabolic efficiency of the wild-type protein CYP2C9\*1 towards phenytoin and (S)-warfarin. Individuals who show dramatically reduced expression of the normal CYP2C9\*1 could show the same hypersensitivity to these drugs.

15 Several factors can affect the basal and induced levels of expression of these genes. For example, mutations or polymorphisms that affect the promoter region of toxic response genes can cause hypersensitivity to compounds. For example, several polymorphisms have been identified in the promoter region of the human HLA-DQA1 gene that affect the levels of mRNA and thus protein levels of the HLA haplotype. Indovina, P.  
20 et al. (Hum. Immunol.) 59(12): 758-67 (1998). Polymorphisms in the regulatory region of the genes encoding plasminogen activating inhibitor increase the risk for developing coronary heart disease (Grenett et al. (Arterioscler. Thromb. Vasc. Biol.) 19(11):1803-1809 (1998). The polymorphisms mentioned above for human plasminogen activating inhibitor are in the regulatory region of the gene and result in altered expression of the gene. This  
25 risk of developing coronary heart disease, and likely increased risk to drugs with cardiotoxic properties, is increased specifically as a function of the altered expression levels. Many toxic stimuli induce or repress TGF- $\beta$ 1 levels. Individuals who overexpress

TGF- $\beta$ 1 show heightened levels of apoptosis and fibrosis seen with mycotoxin-induced liver injury. Cruse et al. (Carcinogenesis) 20(5):817-824 (1999).

5 Polymorphisms in the gene encoding the vitamin D receptor change differential expression of many downstream genes and render the individual likely to develop drug induced psoriasis. Park et al. (Arterioscler Thromb Vasc Biol) 19(11):1803-1809 (1999). Expression levels of the gene for cytochrome P450 CYP1B1 have a strong effect on the susceptibility to 7, 12-dimethylbenz[a]anthracene-induced lymphomas. Thus individuals who do not express appropriate levels of the P450 CYP1B1 gene would be at enhanced risk for toxic side effects of compounds like 7, 12-dimethylbenz[a]anthracene that are 10 metabolized by that P450 protein. Butlers et al. (Proc. Natl. Acad. Sci. USA) 96(5):1977-1982 (1999). Classic quotidian fever was found to be associated with significantly lower levels of plasma IL-6. The published evidence shows that there is a genetically determined difference in the degree of the IL-6 response to stressful stimuli between individuals (Coulthard et al. (Blood) 92(8): 2856-62 (1998)). Thus individuals with genetically linked 15 quotidian fever are likely to be at enhanced risk for a number of drugs that elicit IL-6 expression as part of their inherent toxicity.

The level of expression of the enzyme thiopurine methyltransferase is an important determinant of the metabolism of thiopurines used in the treatment of acute lymphoblastic leukemia and acute myeloid leukemia. TPMT expression displays genetic polymorphism 20 with 10% of individuals having intermediate and one in 300 undetectable levels. Individuals who do not express TPMT are at extreme risk of severe cardiotoxicity when treated with compounds such as azathioprine (Collie-Duguid et al. (Pharmacogenetics) 9(1):37-42 (1999); Coulthard. et al. (Blood) 92(8):2856-62 (1998)). In another example where altered expression of tox-response genes affects the response to specific drugs, 25 experiments have recently demonstrated that overexpression of the human HAP1 protein sensitizes cells to the lethal effect of bioreductive drugs. Prieto-Alamo et al. (Carcinogenesis) 20(3):415-9 (1999).

Altered expression can come from many causes besides mutations in the promoter region. These include, include mutations in the transcription factors or receptors that regulate a gene and gene duplications. While cDNA sequence analysis of a normal sequence that had been duplicated would not detect any change in the coding regions of the genes of interest, gene expression analysis would. For example, two active copies of the X-linked gene spermidine/spermine N1-acetyltransferase (SSAT) in a female lung cancer cell line have been associated with an increase in sensitivity to an anti-tumor polyamine analogue. Mank-Seymour et al. (Clin. Cancer Res.) 4(8): 2003-8 (1998). Duplications in the CYP2D6 or CYP2C19 genes have been shown to be linked with sensitivity to a number of drugs including warfarin, codeine and clofenac. Lundqvist et al. (Gene) 226 (2): 327-38 (1999); Yasar et al. (Biochem. Biophys. Res. Commun.) 254 (3): 628-31 (1999).

There are numerous examples where expression polymorphisms comprise a significant percentage of the population. For example, a genetic polymorphism in the metabolism of the anticonvulsant drug S-mephenytoin has been attributed to defective CYP2C19 alleles. This genetic polymorphism displays large interracial differences with the poor metabolizer (PM) phenotype representing 2-5% of Caucasian and 13-23% of Oriental populations. Ibeanu et al. (J. Pharmacol. Exp. Ther.) 286(3): 1490-5 (1998). Several individuals showing poor metabolic capacity to coumarin and (+)-cis-3,5-dimethyl-2-(3-pyridyl)thiazolidin-4-one hydrochloride show very low levels of the CYP2A6 gene product. See Nunoya et al. (Pharmacogenetics) 8(3):239-49 (1998).

There are multiple additional examples of reported variation in genes known to be important in toxic responses, but clinical investigation has not yet been performed to determine their relative susceptibility to specific drugs. The human UDP-glucuronosyltransferase (UGT1A) locus is regulated in a tissue specific fashion in liver and extrahepatic tissues. Activity assays demonstrated 2- to 4-fold inter-individual differences in UGT activity and qualitative differences between individuals. The polymorphic regulation of UGT1A gene products in gastric tissue may be the biological basis that

determines inter-individual differences in extrahepatic microsomal drug metabolism.  
Strassburg et al. (Mol. Pharmacol.) 54(4):647-54 (1998).

Very importantly, it is likely that many mutations in single genes result in altered expression of many more genes, an amplification effect. A knock-out mutant has been  
5 created in mice that destroyed the function of a single gene, the au-beta 6 gene. The resulting animals showed altered basal expression of 101 genes in lung epithelial cells.  
Kaminski et al. (New York Academy of Sciences meeting, Toxicology for the Next Millenium, Airlie VA, USA) September 1999.

Single mutations in any one of hundreds of key toxicity genes can potentially cause  
10 differential basal levels of expression of many additional genes. It may be the altered expression of these genes that render the cell, or organism sensitive to toxic stress, not the initial mutation by itself.

Gene expression analysis has been used to predict who will respond beneficially to the therapeutic effects of treatments. The levels of Bax and Bcl-2 expression after  
15 radiotherapy have been used as prognostic markers in patients with human cervical carcinoma. Harima et al. (J Cancer Res Clin Oncol 124(9): 503-10. (1998). In acute myeloid leukemia, coexpression of at least two proteins, including P-glycoprotein, the multi-drug resistance-related protein, bcl-2, mutant p53, and heat-shock protein 27, have been reported to be predictive of the response to chemotherapy. Kasimir-Bauer et al. (Exp  
20 Hematol) 26(12): 1111-7 (1998). The work by Kasimir-Bauer et al. shows that gene expression profiling can be used to predict who will benefit from the therapeutic effects of a drug; it does not address the question as to who will suffer enhanced toxicity of a drug.

All of the above examples show that altered levels of gene expression of a certain set of tox-response genes are associated with qualitatively or quantitatively distinct  
25 responses to the toxic effect of different drugs. Many of the examples show that DNA sequence polymorphisms would not be sufficient to predict hypersensitive individuals. Finally, the disclosure and examples herein show that measurement of a multiple set of tox-

response genes will reveal patterns of gene expression that will identify hypersensitive individuals for specific types of toxicity.

Experimental Identification of Genes

5       Genes associated with hypersensitivity to an agent may be identified in a variety of ways experimentally. Generally the expression of genes that are differentially expressed in total across cell, organ and tissue types in humans, in particular in response to toxic insult is evaluated to determine genes associated with hypersensitivity in an individual. In one embodiment, a method of identifying genes associated with hypersensitivity to an agent is  
10      provided, that comprises comparing the gene expression profile of cells treated with an agent with the gene expression profile of untreated cells, and determining genes in the treated cells that have altered expression due to the treatment, thereby to identify one or more genes associated with hypersensitivity to the agent. The cells may comprise one or more different cell types, wherein each said cell type comprises a gene associated with  
15      hypersensitivity to the agent. Alternately, the cell types are derived from a single tissue or organ.

Exemplary cell types are those derived from a specific organ , cell or tissue, such as kidney, liver, lung, heart, breast, lymphocytes, neuronal cells, skin, or intestine, such as HepG2, Caco-2, MCF-7, Jurkat, Daudi, HL-60, MCL-5, SKBR-3, SKOV-3, PC-3, WISH  
20      and HeLa.

Another method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent comprises comparing the gene expression profile of multiple cell types of an individual known to be hypersensitive to an agent with the gene expression profile of said cell types in an individual known not to be  
25      hypersensitive to the agent; and identifying genes from said multiple cell types having a pattern of differential gene expression, wherein the pattern of differential gene expression is associated with hypersensitivity to the agent.

An alternative to this method comprises, comparing the gene expression profile of multiple cell types of an individual known to be hypersensitive to an agent before treatment with the agent with the gene expression profile of multiple cell types of the hypersensitive individual after treatment with the agent, and identifying genes from the multiple cell types having a pattern of differential gene expression, wherein the pattern of differential gene expression is associated with hypersensitivity to the agent.

When normal or hypersensitive animals, humans or cells are exposed to a selected agent, gene expression changes can be analyzed in genes such as those listed in Table 3, 4, 5, 6, 8, 10 and 11. Different types of toxic insult lead to different patterns of gene expression changes in normal, as well as in hypersensitive individuals. Since substantially all compounds elicit toxicity at a high enough dose, the mechanisms of drug toxicity in normal individuals has been well examined. Genes that cells induce to combat the toxic effect of various compounds are important for anti-toxicity for each compound. Patterns of gene expression of these genes in individuals who show hypersensitivity to a given compound that differ from the pattern of differential expression of normal individuals, with or without treatment can be identified. Using these methods, sets of genes that have characteristic expression in hypersensitive individuals that differs from normal individuals may be identified.

Subsets of genes and expression profiles thereof that can be used to identify hypersensitive individuals are identified as follows. A technique such as amplified fragment length polymorphism (AFLP) or serial analysis of gene expression (SAGE), which are known in the art, is used to compare gene expression profiles from treated and untreated human cells. The agent is administered at a toxic dose. This procedure identifies all candidate genes within the cells that respond to the toxic stimuli posed by a particular agent. The method further comprises using a technique, such as AFLP or SAGE, which are known in the art, to compare the gene expression profiles from treated and untreated normal cells. This step would identifies all genes within an individual that respond to that

agent. It also permits investigators to understand the normal expression range of individuals who are not hypersensitive. A technique, such as AFLP or SAGE, is used to compare gene expression profiles for samples from treated and untreated hypersensitive individuals or cell cultures derived therefrom. This step identifies all genes within 5 hypersensitive individuals that respond to the treatment by that agent. It also allows investigators to understand the expression range of hypersensitive individuals. This permits identification of the genes that were differentially expressed in all of the above experiments, thus eliminating genes associated with therapeutically beneficial effects and individual variation in expression of genes unrelated to the compound. The expression of 10 these genes can then be measured in a larger population of normal and hypersensitive individuals using, for example gene arrays, RT-PCR or other techniques known in the art to confirm the correlation between those genes identified in the above procedures and hypersensitivity observed in particular individuals.

Gene expression responses to toxic stimuli can be analyzed using a database of 15 information. The first method is to determine which genes are induced and what is their function. For example, if all genes induced by a compound are regulated by DNA damage, the interpretation is that the compound causes DNA damage. This interpretation requires a database about the function and regulation of all genes in the database. Another method of interpretation is to determine whether the gene expression pattern induced by a second 20 compound is similar to that induced by a compound, the toxicity of which is well-characterized. This approach to interpretation requires an extensive database of gene expression profiles generated from well-characterized compounds. Table 7 shows a partial list of well-characterized compounds for which gene expression data has been generated.

The methods of gene expression analysis discussed herein can be performed using a 25 computer system with computer code suitable for accessing and comparing the gene expression profile determined according to the methods of this invention. Suitable software will also rank the results of these analyses. Computer code suitable for these

purposes can be programmed by a person skilled in the art. Exemplary software and a gene expression profile database related to toxicology are commercially available from Phase-1 Molecular Toxicology, (Santa Fe, NM), for example, Chem Profiler<sup>TM</sup> and Matrix Express<sup>TM</sup>.

5

Examples of Genes Associated with Hypersensitivity

Several drugs have been shown to elicit allergic reactions in a subset of the population. The more extreme form of these allergic reactions can be quite severe and involve extensive damage of significant portions of the skin covering the body. Many 10 patients die from dehydration and infection. The extreme form of these allergic reactions have the names Steven Johnson Syndrome and TEN (Toxic Epidermal Necrosis). Drugs known to elicit Steven Johnson Syndrome and TEN and less severe forms of skin allergy include navirapine, dapsone, acebutolol, trimethoprim, sulfasalazine, sulfacetamide, sulfadiazine, sulfamethoxizole, sulfasoxazole, sulfamethizole cotrimoxazole, amoxicillin, 15 phenytoin, sulfonamide and penicillin.

Gene expression data suggests that the expression levels of a relatively small number of genes can identify who will develop allergic reactions to these drugs. The genes whose expression in CD8 T Cells and keratinocytes is likely to identify hypersensitive individuals include: inducible NOS, Ki-67, Transglutaminase-1, IL-1, FASL, TNF-alpha, 20 CD11b/CD18, p75-R-TNF (TNF Receptor), IL-6 receptor, G-CSF receptor, HSP-70, INF-gamma, ICAM-1, VCAM-1, ECAM-1, and TGF-beta.

While not being limited to any theory, it is believed that there is a similar molecular mechanism for both Steven Johnson Syndrome and TEN. The invention provides a method to determine who will develop these syndromes prior to taking these drugs.

25 All publications, patents, and patent applications referred to herein are incorporated herein by reference.

The following examples are intended to illustrate but not to limit the invention.

## EXAMPLES

5

### Example 1: Identification of Genes Associated with Hypersensitivity and Screening of Subjects Prior to Drug Administration

Initially, one or more compounds predetermined to cause blood toxicity, such as agranulocytosis, in at least 4% of the patient population, are chosen, e.g. Haldol<sup>TM</sup> (haloperidol). The differential gene expression profile associated with Haldol<sup>TM</sup> (haloperidol) is determined in neutrophils from both normal and hypersensitive subjects when exposed to high concentrations of Haldol<sup>TM</sup> (haloperidol). The gene expression profile from untreated and treated cells is compared using for example, AFLP, a microarray of the genes listed in Tables 3 and 4, or SAGE, to identify genes that vary as a function of toxicity and vary as a function of hypersensitivity to the Haldol<sup>TM</sup> (haloperidol). Next, 10 gene expression from clinical samples from a patient population exposed to Haldol<sup>TM</sup> (haloperidol) or a placebo is measured. The clinical samples are provided by the manufacturer of Haldol<sup>TM</sup> (Hoechst Marion Roussel). Genes are identified that co-varied with the hypersensitivity status. Additional clinical samples are blinded and provided by 15 the manufacturer which includes samples from normal and hypersensitive subjects. Using the present invention, prediction of the hypersensitivity status is based upon gene expression profiles. The level of accuracy of the prediction or correct identification is determined by unblinding the compounds.

20

In the final stage, gene expression analysis of the key set of genes would be performed on a prospective basis with new patients just beginning treatment with Haldol. The level of accuracy of the prediction or correct identification of hypersensitivity is 25 determined by monitoring patients over time to see if those predicted to develop

agranulocytosis indeed did so. This empirical approach is then be extended to other drugs and other drug manufacturers.

Example 2: cDNA Probe Production

5 A fluorescent dye labeled cDNA probe complementary to the mRNA component of cellular RNA harvested from cells exposed to toxicologic challenge is produced by this protocol, which is designed to produce sufficient Cy3 labeled probe from one experimental sample, and Cy5 labeled probe from one control sample, to develop one microarray slide. The procedure is scalable to easily accommodate, for example, 16 samples. This will  
10 produce sufficient probe mixtures for at least 8 microarray slides. General procedures as described, for example, in Gerard et al. (Focus®) 14:91 (1992); Kotewitz et al. (Gene) 35: 249 (1985); and Gerard et al. (DNA) 5: 271 (1986) are utilized.

15 cDNA probes may be used in an assay for detecting expression of genes associated with hypersensitivity to an agent. In one embodiment, microarray slides are provided that contain ssDNA sequences, or targets, from a number of toxicologically relevant genes. The microarray slides, for example, may be 3"x 1" glass microscope slides comprising an array of micron-scale spots of ssDNA sequences on the upper face. The DNA may be bound to the slide using covalent linkage chemistries known in the art.

20 Total RNA from cells contains mRNA species that are homologous to these sequences. "Total RNA (high quality)" refers to substantially total cellular RNA. As RNA is very labile, special care must be taken to insure that it is of sufficient integrity at the time of use as template in the production of probe. The level of these mRNA species is proportional to the degree of induction of the gene by the agent under study. This protocol describes the production of fluorescent labeled cDNA probe from the total RNA of cells  
25 which have either been exposed to the agent under study, or are serving as a non-treated control. These probes are then pooled and hybridized to the microarray slide. The experimental and control probes are distinguishable because the Cy3 and Cy5 labels

fluoresce at different wavelengths. The degree to which each probe binds to a specific gene sequence on the slide reveals the level of induction of that gene in the cells exposed to the agent under study.

5      The following materials are used:

	<u>Material</u>	<u>Amount</u>	<u>Exemplary Source</u>
	DEPC treated water	10ml	Ambion®
10	Alk Water (pH 7.5 with NaOH)	1ml	
	Total RNA (of high quality) or Messenger RNA (of high quality)	10µg/sample	
	First strand buffer	2µl/sample	
	0.1 M DTT	4µl/sample	Sigma®
15	1:8 dilution Cy3 dCTP (3-amino-propargyl-2'-deoxycytidine 5'-triphosphate) (i.e., 0.125mM Cy3 dCTP)	2µl/sample	Amersham®
	1:10 dilution Cy5 dCTP (3-amino-propargyl-2'-deoxycytidine 5'-triphosphate) (i.e., 0.1mM Cy5 dCTP)	1µl/exp. Sample	
20	SuperscriptII (RT)	1µl/sample	Amersham®
	ANTI-RNase	1µl/sample	Life Technologies, Inc.
	7.5 M ammonium acetate	34µl/sample	Ambion®
	70% EtOH	1ml/sample	Sigma®
	95% EtOH	220µl/sample	J. T. Baker®
25	Nucleotide Mix "3"	1µl/exp. sample	J. T. Baker®
		0.5 mM dATP/dGTP/dTTP	
		0.125 mM dCTP	
	Nucleotide Mix "5"	1µl/control sample	
		0.5 mM dATP/dGTP/dTTP	
30	Stock anchored oligo dT:	0.15 mM dCTP	
		4µl/sample	
		0.25µg/ml of each oligo dT	
	RNase Zap	(in Water @ -20°C)	
35	Wet ice	(1) bottle The RNA Co.™	
	Qiagen Qiaquick PCR purification kit	(1) bucket	
	PE/ETOH	(1) ea Qiagen®	
	EB Buffer	(1) bottle	
		(100 ml PE buffer + 400 ml >96% EtOH)	
		10 ml (10 mM Tris-HCl pH 8.5)	

General Protocol

5 Steps are performed at room temperature unless otherwise specified. Work areas are cleaned and swabbed with RNase Zap. Gloves are worn at all times. RNase (RNA specific endo-and exo-nucleases) is a ubiquitous and very stable enzyme. Standard cleaning and/or autoclaving will not remove or inactivate it. Therefore all materials contacting the samples must be known RNase-free. All water, including for buffers, must be DEPC-treated. DEPC treatment consists of an autoclaved solution of 0.1% Diethyl pyrocarbanate in de-ionized water.

10 Preparation of RNA template in water is implemented by adjusting mRNA to a concentration of 2 $\mu$ g/7 $\mu$ l or total RNA to a concentration of 10 $\mu$ g/7 $\mu$ l for each sample in a standard microfuge tube. If concentration adjustment requires dehydration in the Speedvac™, 1  $\mu$ l Anti-RNase is added prior to dehydration. The reaction solution is prepared by adding 4  $\mu$ l of stock anchored oligo dT per tube, heating at 70°C for 10 minutes in a heat block, spinning 5 seconds in microfuge, and placing on ice for 2 minutes.

15 The following is then added to each tube:

4  $\mu$ l 5x First Strand Buffer for SuperscriptII

2  $\mu$ l 0.1 M DTT

and either (for treated samples):

1  $\mu$ l Nucleotide Mix “3”

20 1  $\mu$ l of 1:8 dilution of Cy3

or (for control samples):

1  $\mu$ l Nucleotide Mix “5”

1  $\mu$ l of 1:10 dilution of Cy5.

25 The tube then is incubated at room temperature for 10 min. The dCTP is added to limit the concentration of Cy dCTPs incorporated. Due to the size of the Cy dCTP, the polymerase will fall off the template if more than two are incorporated in a row.

To perform the reaction, 1  $\mu$ l SuperScriptII is added to each tube, and the contents mixed gently. The tube then is incubated for 1.5-2 hr. at 45°C in a heat block, keeping the reaction protected from light. The fluorescent dyes Cy3 and Cy5 are sensitive to light. Excessive exposure during processing will reduce the intensity of emission upon final scanning.

5 To collect the labeled cDNA probe, ethanol precipitation is implemented by adding to each tube 46 $\mu$ l of water, 34 $\mu$ l of 7.5M ammonium acetate and 220 $\mu$ l of 95% EtOH, and then incubating at -80°C for 15-20 min. If desired, procedure may be interrupted at this point. The sample may be stored at -80°C for up to 7 days.

10 The tubes are loaded in centrifuge with orientation of lid noted, centrifuged for 15 min at 20800 x g, and the supernatant discarded, to obtain a visible pellet (pink for Cy3, blue for Cy5). The pellet is washed by adding 750 $\mu$ l 70% EtOH per tube and vortexing briefly, centrifuging at 20800 x g for 10 min, decanting and discarding the supernatant, centrifuging the pellet and optionally gently removing remaining EtOH with a pipette, 15 while being careful not to loosen the pellets. The pellet is allowed to dry for 10 min. at room temp, but not over drying by using a vacuum, and resuspended in 40 $\mu$ l water. cDNA/mRNA hybrid is denatured by incubating at 95°C for 5 min. in a heat block. The tube then is spun 5 seconds in microfuge.

20 The labeled cDNA probe is purified in an adaptation of the procedure described on page 18 of the QIAquick Spin Handbook, (1997) Qiagen®. To bind the cDNA probe to a column, 200  $\mu$ l of Buffer PB is added to each 40 $\mu$ l probe solution, the QIAquick spin columns are placed in 2 ml collection tubes, and the samples are applied to the QIAquick columns and centrifuged at 10,000 x g for 2 min. The flow-through is discarded and QIAquick columns replaced into the same tubes.

25 To wash bound cDNA probe, 750 $\mu$ l Buffer PE/ETOH is added to each column, and the column incubated for 1 min. at room temp. The column is centrifuged at 10,000 x g for 2 min., and the supernatant discarded. The wash is repeated. QIAquick columns are

placed back in the same tubes, and centrifuged for an additional 1 min at maximum speed with tube lids open. Residual ethanol from Buffer PE will not be completely removed unless the flow-through is discarded before this additional centrifugation.

QIAquick columns are placed in clean 1.5ml microfuge tubes. To elute the cDNA probe, 40 $\mu$ l (+/- 10 $\mu$ l) Alk. Water is added to the center of each column. The tubes are 5 incubated for 1 min, centrifuge at 6000 x g for 1 min., and the elution steps repeated once into same tube. The elution buffer is dispensed directly onto the QIAquick membrane for complete elution of bound cDNA.

To quantify the cDNA probe, each sample is put in ~80 $\mu$ l of EB buffer, and 10 transferred to one well of a 384 well plate. Scanning, including the measurement and recording of the type and degree of fluorescence from each spot on a processed microarray slide, is accomplished in a confocal laser scanning fluorimeter. The fluorimeter is set to the appropriate excitation/emission frequencies and records the level of emission for the sample. The exposure time and intensity is controlled, because exposure of the label to 15 strong light incrementally reduces its fluorescent activity. Values from this procedure are the result of many variable factors. Therefore it is preferable to compare to an archive of values produced from the same procedure and equipment.

To prepare the final probe mixture, the Cy3 labeled experimental probe is combined with the Cy5 labeled control probe. If a control requires multiple reactions, they are 20 combined prior to aliquoting equal amounts to the experimental samples. The combined probes are concentrated to ~1 $\mu$ l in a Speedvac at a temperature not exceeding 45°C. If the probe is not used immediately, 10  $\mu$ l water is added and it is stored at 4°C.

Example 3: Determination Of Gene Expression Changes Associated With Toxicity

25 To determine genes useful for identifying patterns of genes associated with toxicity, animals were exposed to concentrations of selected compounds that elicit peroxisome proliferation, a type of liver toxicity. Treatments were with WY 14,643, gemfibrozil and

clofibrate in Sprague Dawley rats. Each compound was administered in 1% carboxymethylcellulose/0.2% Tween 80 by oral gavage daily for 14 days. Administered doses were to three animals per dose per time point as follows; WY14,643, 40 mg/kg/day; gemfibrozil, 24 mg/kg/day and 100 mg/kg/day, and clofibrate 40 mg/kg/day and 250 mg/kg/day.

Gene induction was measured using microarrays consisting of 250 toxicologically relevant rat genes using the hybridization protocol described above. As illustrated in Figure 4, several genes were induced by the treatment, example given is for WY14,643. This figure shows a gene expression profile showing the relative induction levels compared to untreated controls. As shown in Figure 4, the genes referred to in Figure 4 as A (Cytochrome p450 4A *CYP4A*, B (Enoyl Co-A Hydratase), C (3-ketoacyl CoA thiolase 2), D (Acyl CoA Oxidase), and E (Ketoacyl CoA thiolase type 1), had enhanced expression in comparison to the control after treatment with the compound. These genes were found to be induced by a variety of other peroxisome proliferating agents including gemfibrozil, clofibrate, fenofibrate and DEHP. This set of genes was thus empirically shown to be induced by a variety of compounds that exhibit a specific type of hepatotoxicity, peroxisome proliferation. By way of example, individuals who display hypersensitivity to these types of compounds should show altered expression of this set of genes.

20      Example 4: Probe For Hepatocyte Growth Factor

New genes associated with and predictive of toxicity were identified. Different types of damage to the liver cause the formation of dead and dying hepatocytes, which the liver replaces to maintain its function. Induction of the hepatocyte growth factor receptor gene by toxic stimuli in both rats and humans was examined. When several nitrosoureas including streptozotocin, carmustine and MNU were used to determine gene expression profiles, all of these compounds induced several genes in common. These compounds are all known to form covalent adducts to the DNA in liver and liver cells. All compounds, for

example induce both the hepatocyte growth factor receptor gene and the glutathione transferase gene. Exemplary data is provided in Figure 1 which shows the gene expression profile in the liver of male Sprague-Dawley rats when treated with the hepatotoxicant streptozotocin.

5       The probe for the hepatocyte growth factor receptor gene was created by cloning at least a 250 base-pair section from the 3' coding region of the gene starting with total genomic DNA. The fragment was derived by PCR from genomic DNA using two primer with appropriate linkers for insertion into a plasmid vector. A single stranded probe complementary to the cDNA sequence was attached to a glass slide array using a  
10 polyamine attachment.

In more detail, an example of creation of a specific probe for the hepatocyte growth factor receptor is as follows. The first step in the process is obtaining the sequence for the gene. The search for gene sequence, either by gene name or accession number, is performed using the NIH National Center for Biotechnology Information website using  
15 Genbank ([http://www2.ncbi.nlm.nih.gov/genbank/query\\_form.html](http://www2.ncbi.nlm.nih.gov/genbank/query_form.html)). The accession number for the rat hepatocyte growth factor receptor gene is X96786. When the sequence of interest is located, the sequence information is copied to a Microsoft Word file. Intron sequences are then removed, if present, as well as numbers and white spaces. The resulting condensed sequence is then submitted to a PCR primer design software program, such as  
20 Primer3 (<http://www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>). Primers are selected that optimally have a  $T_m$  in the range of 60°-63°C. The optimal length of the gene fragment is 500 bp. Shorter fragments are chosen if the starting sequence is shorter than 500 bp.  
Once the primers are designed, the sequence that is flanked by the primers is submitted to a BLAST search. BLAST (Altschul et al (Nucleic Acid Res) 25: 3389-3402. (1997)) is a  
25 sequence analysis software program supported by the NIH. The BLAST search software searches for other DNA sequences that are homologous to the target sequence and ranks these sequences according to the amount of homology. This ensures that the chosen gene

fragment sequence will not cross-hybridize with a gene sequence other than the desired sequence. PCR primers are ordered and an attempt is made to isolate the gene fragment from a cDNA library that is created by reverse transcription of RNA from either a cell line(H4IIE) or rat tissue. Upon identification of a PCR band of the correct size, the PCR  
5 product is cloned into a vector (TA cloning vector, Invitrogen Corp., Carlsbad, CA). Following cloning, a bacterial mini-prep is performed to amplify and isolate the plasmid containing the gene fragment of interest. The region of the plasmid containing the gene fragment is then sequenced. If this sequence matches the original target sequence, the target sequence of this clone is amplified by PCR, purified (Wizard system, Promega  
10 Corp., Madison, WI), quantified, and used for spotting.

The probe refers to a population of cDNAs bearing fluorescently active ligands which are produced from the mRNA of the cells under examination, while "probe mixture" refers to a mixture of two or more populations of cDNA. The cDNAs may also be labeled with a variety of ligands, such as fluorescently active ligands, radioisotope ligands or  
15 biotinylated ligands.

#### Example 5: Glutathione Transferase Positive Foci

Enhanced gene expression and co-induction of genes associated with the formation  
20 glutathione transferase positive foci was identified.

Certain types of toxic liver damage produce glutathione transferase positive foci Lemmer et al. (Carcinogenesis) 20:817-824 (1999) which are cells that are in the late stages of dying. In response, neighboring hepatocytes must replicate in order to replace the dying cells and induce expression of hepatocyte growth factor so that they are 'primed' for  
25 growth hormone signals.

Co-induction of the glutathione transferase and hepatocyte growth factor receptor genes was determined by hybridization to microarrays containing at least 300 human toxicologically relevant genes using the hybridization protocols described above.

Figure 2 is a graph showing the results, which indicated a very strong correlation between the induction of the glutathione transferase and hepatocyte growth factor receptor genes. Co-induction thus shows correlation to focal cell death occurring in the liver.

Example 6: Heart Muscle Tissue Gene Expression Profile

Animals were exposed to doxorubicin, a cardiotoxin. Male Sprague-Dawley rats were treated with 1 mg/kg doxorubicin in 5% saline for 6 to 24 hours, and 7 days and 6 weeks with one dose per day and a 6 week recovery period. A gene expression profile of heart muscle tissue cells was then obtained. RNA was isolated and the gene expression profile was analyzed as described below. Gene expression of all genes listed in Table 8 was determined. The results of the gene expression of the first 66 genes is shown in Figure 3.

As can be seen from Figure 3 and Table 8, several genes, including activating transcription factor 4, activin receptor type II, ataxia telangiectasia, c-jun, carnitine palmitoyl-CoA transferase, DNA Dependent helicase, Epoxide hydrolase, farnesol receptor, Gadd 45, Interleukin 6, MDM-2, Ribonucleotide reductase subunit M1 and at least 10 others were differentially expressed at significant levels. Many of these genes, including Carnitine Palmitoyl transferase, Epoxide hydrolase, Farnesol receptor, Lipoprotein lipase precursor, and MDM-2 have never been reported or previously known to be induced by cardiotoxicity.

Thus a profile of gene expression characteristic of the cardiotoxin, doxorubicin was obtained. Genes thus identified as having altered expression in the presence of cardiotoxin are significant, because individuals with diminished or altered expression of the induced genes may potentially be hypersensitive to the toxicity of doxorubicin. Such

hypersensitivity could manifest itself at the molecular level as altered induction of these genes as well as a shift in the dose-response curve such that the same genes would be induced at lower concentrations.

5      Example 7 Determining genes associated with hypersensitive reaction to penicillin

Three different methods, differential display, microarray technology, and Taqman® assay were used to determine genes associated with hypersensitive reaction to penicillin. Seven self-described penicillin-sensitive individuals and six individuals self-described to have normal reaction to penicillin were tested by differential display. Six self-described 10 penicillin-sensitive individuals and six individuals self-described to have normal reaction to penicillin were tested by microarray technology.

1. Lymphocyte culture

15      Six individuals self-described as penicillin sensitive and seven individuals self-described as having normal reaction to penicillin were used to determine potential hypersensitive reactions to penicillin in humans. Peripheral blood leukocytes (PBL) were isolated from a population of individuals, cultured with PHA at a standard concentration for culturing lymphocytes for 24 hours, washed, cultured for another 24 hours without 20 PHA, and divided into two groups. One group was exposed to penicillin *in vitro* for 24 hours and the other group was not exposed to penicillin as a control group. At a non-toxic dose of 1250 µg/ml, penicillin G is known to elicit an immune response in peripheral blood of individuals with proven penicillin G allergy.

25      2. Isolation of RNA from cultured lymphocytes

RNA from select individual from both groups (treated and untreated) of cultured lymphocytes was isolated as follows. Total RNA of high quality and high purity is isolated from cultured cells by using Qiagen QIAamp® RNA blood mini kit and 2-

mercaptoethanol. RNA degradation by RNases is not desirable when synthesizing fluorescent cDNA for hybridization with the penicillin array. Precautions are taken to minimize the risk of RNA degradation by RNases by wearing gloves, treating work areas and equipment with a RNase inhibitor, for example, RNase Zap (Ambion® Products, 5 Austin, TX) and keeping samples on ice. This total RNA isolation technique is based on a Qiagen QIAamp®RNA blood mini kit and is used with some modification for human lymphocyte cells in a T-75 flask.

Cells are checked under the microscope to make sure that they are viable. Cells are dosed with penicillin on the third day in culture (48 hours after introduction of the cells into 10 culture).

Cells are scraped from the flask and poured into a 50 ml conical tube. The flask is then rinsed with 10 ml of room temperature PBS. The PBS wash is removed with a pipette. The tube is then spun for 10 minutes at 1,000 rpm and the supernatant pipeted off. The remaining pellet is resuspended in 600 $\mu$ l of freshly prepared RLT buffer (RLT buffer 15 requires the addition of 10 $\mu$ l of beta mercaptoethanol for each 1.0 ml RLT) by vortexing. The resuspended pellet is pipeted into a QIAshredder® column and centrifuged for 2 minutes at 14,000 rpm in a Eppendorf® 5417C centrifuge. The QIAshredder® column is discarded and 600  $\mu$ l of 70% ethanol added to the lysate. The lysate is then pipeted into a QIAamp® spin column sitting in a 2 ml collection tube and centrifuged for 15 seconds at 20 14,000 rpm. Any remaining lysate is placed on the same column and the centrifugation is repeated. The QIAamp® spin column with the RNA bound to the column is transferred to a new 2 ml collection tube. 700 $\mu$ l of Qiagen® RW1 buffer is added to wash the column and centrifuged for 15 seconds at 14,000 rpm. The QIAamp® spin column is transferred to a new 2 ml collection tube. 500 $\mu$ l of Qiagen® RPE buffer is added to the column and 25 centrifuged for 15 seconds at 14,000 rpm. The QIAamp® spin column is transferred to a new 2 ml collection tube. 500 $\mu$ l of Qiagen® RPE buffer is added to the column and centrifuged for 3 minutes at 14,000 rpm. The QIAamp® spin column is transferred to a

new 2 ml collection tube and centrifuged for 1 minute at 14,000 rpm. The QIAamp® column is transferred to 1.5 ml microcentrifuge tube and 50 µl of RNase-free water is added to the column and centrifuged for 1 minute at 14,000 rpm. An additional 50 µl of RNase-free water is added to the column and centrifuged for another 1 minute at 14,000

5 rpm.

To measure the yield, the O.D. reading is taken at 260nm on a Beckman DU®350 UV vis spectrophotometer. 1.0 µl RNA is added to 49 µl of sterile nanopure water and the O.D. reading is taken and calculated as follows:

$$(Absorbance) \times (\text{dilution factor}) \times (40)/1000 = \text{amount of RNA in } \mu\text{g}/\mu\text{l}$$

10 Example: absorbance = 0.45

Dilution factor = 50

$$\underline{(0.45) \times 50 \times 40} = \text{RNA concentration in } \mu\text{g}/\mu\text{l}$$

1000

The sample is stored in -80°C freezer.

15

### 3. MessageClean® of Total RNA

It is important that total RNA that is used to make mRNA differential display is absolutely free of DNA contamination. Regardless of the method used for RNA isolation, a cleaning step is important to ensure the removal of DNA contamination, especially if the 20 differential display banding pattern on the denaturing polyacrylamide gel is independent of the reverse transcription step. MessageClean® from GenHunter (Nashville, TN) was used to clean total RNA. Components for twenty RNA sample cleanings included the following materials: 140 µl 10x Reaction Buffer, 20 µl GH-DNase I (RNase free, 10 units/µl), 140 µl 3M NaOAc, and 1 mL DEPC-treated H<sub>2</sub>O. For DNase I digestion, the following materials 25 were added in order: 50 µl total RNA (10-50 µg), 5.7 µl 10x Reaction Buffer, 1 µl DNase I (10 units/µl) for a total volume of 56.7 µl. The materials were mixed well and incubated at 37 degrees for 30 minutes. A 3:1 phenol/chloroform mixture is used to ensure removal of

protein contamination and DNase I from the RNA. About 40  $\mu$ l of phenol/chloroform is added to the mixture, vortexed for 30 seconds, and allowed to sit on ice for about 10 minutes. Then the mixture was spun in an Eppendorf centrifuge at 4 degrees for 5 minutes at maximum speed and the upper phase of the mixture is collected. Ethanol precipitations was performed as follows. About 5  $\mu$ l of 3M NaOAc and 200  $\mu$ l of 100% ethanol was added to the upper phase that was collected. This was placed at -80 degrees for more than 1 hour and then spun for 10 minutes at 4 degrees. The supernatant was removed, the RNA pellet was washed with 0.5 mL of 70% ethanol (in DEPC-treated water), and spun for 5 minutes to remove the ethanol. The tube containing the materials were spun again and the residual liquid was removed. The RNA was re-dissolved in 10-20  $\mu$ l DEPC-treated water. The RNA was quantitated by reading on a spectrophotometer at OD<sub>260</sub>. RNA that is diluted for any purpose, such as quantitation, should not be re-used after freezing and thawing. The integrity of the RNA can be checked by running a few micrograms on a 7% formaldehyde agarose gel and looking for the clear appearance of 28S and 18S rRNA bands.

#### 4. Reverse transcription

In a tube, the following ingredients are added: 9.4  $\mu$ l dH<sub>2</sub>O, 4.0  $\mu$ l 5x RT buffer, 1.6  $\mu$ l dNTP (250  $\mu$ M), 2.0  $\mu$ l of 0.1  $\mu$ g/ $\mu$ l freshly diluted total RNA that is DNase-free, 2.0  $\mu$ l H-T<sub>11</sub>M (2  $\mu$ M) for a total volume of 19  $\mu$ l. The ingredients are mixed well and incubated at 65°C for 5 minutes, 37°C for 60 minutes, 75°C for 5 minutes, and held at 4°C. After the tubes had been at 37°C for 10 minutes, and 1  $\mu$ l of SuperScript II reverse transcriptase (Life Technologies Inc.) is added to each reaction, and quickly mixed by finger tapping the tubes before the incubation continued. At the end of the reverse transcription, the tubes are spun briefly to collect condensation. The tubes are set on ice for PCR or stored at -20°C for later use.

5. PCR to amplify gel band

The following is an exemplary protocol for PCR. The following ingredients are used: 10 µl dH<sub>2</sub>O, 2 µl 10x PCR buffer, 1.6 µl DNTP (25 µm), 2 µl of 2 µm H-AP primer, 2 µl of 2 µm H-T<sub>11</sub>M, 2 µl RT-mix described above (must contain the same H-T<sub>11</sub>M used for PCR), 0.2 µl α-<sup>33</sup>p DATP (2000 ci/mmole), 0.2 µl TAQ DNA polymerase from PE Biosystems for a total volume of 20 µl. The tube containing all these ingredients are mixed well by pipeting up and down and placed in a thermocycler at 95°C for 5 minutes and then amplified for 40 cycles under the conditions of 94°C for 30 seconds, 40°C for 2 minutes, 72°C for 30 seconds and finally held at 4°C until the samples are removed from the thermocycler.

6. Gel electrophoresis

RNA was analyzed by gel electrophoresis to identify possible candidate genes. A 6% denaturing polyacrylamide gel in TBE is prepared and allowed to polymerize for at least 2 hours before using. Then the gel is run for about 30 minutes before any samples are loaded. It is important for all the sample wells in the gel to be flushed and cleared of all urea prior to loading any samples in the wells. About 3.5 µl of each sample is mixed with 2 µl of loading dye and incubated at 80°C for 2 minutes immediately before loading onto the 6% gel. In this example, the loading dye is xylene and after the gel is loaded with the samples obtained from the rounds of PCR, the gel is run at 60 watts of constant power until the xylene dye is about 6 inches from the bottom of the gel. Once the power is turned off, the gel is blotted onto a large sheet of exposed autoradiograph film. The gel is covered with plastic wrap and under dark conditions, the gel is placed in a large autoradiograph cassette with a new sheet of unexposed film, marked for orientation, and the film is allowed to be exposed to the gel at -80°C. The exposure period can be anywhere from overnight to 72 hours. Once the film has been developed, bands of interest, which show differential expression between penicillin sensitive and normal individuals, are identified by alignment

with the developed film and subsequently isolated by cutting the band of interest out of the polyacrylamide gel with a clean scalpel blade. The isolated band is placed in 100 µl of water and boiled at 95% for 5 minutes.

5      7. Cloning re-amplified PCR products for differential display

The following procedure was used to clone re-amplified PCR products from differential display. Material which may be used include the PCR-TRAP® Cloning System (GenHunter®). For a 20ul Ligation reaction, add in order: 10ul dH2O; 2ul 10X ligase buffer; 2ul Insert-ready PCR-TRAP® Vector; 5ul PCR product; 1ul T4 DNA ligase.

10     The reaction is mixed well by finger tipping and is briefly spun. Then the reaction is ligated overnight at 16°C. The reaction can then be used directly for transformation or stored at -20°C. For transformation, the GH-competent cells are thawed in ice water slush for 15 minutes. While the cells are melting, the appropriate number of 1.5ml microfuge tubes are labeled and set on ice. The cells are quickly mixed by finger tipping and are

15     divided into 100ul aliquots into each 1.5ml microfuge tube. The remaining competent cells are immediately re-frozen for future use. The ligation tubes are spun briefly to collect condensation. About 10ul of each ligation mix is added to an above tube containing the competent cells and mixed well by finger tipping and incubated on ice for 2 minutes.

20     About 0.4ml of LB medium is added and the cells are incubated at 37°C for 1 hour. It is important that no Tetracycline be in the LB during this step because the bacteria with recombinant plasmids need time to express the Tetracycline resistance gene. It is recommended that the LB-Tet plates are warmed at 37°C for 1 hour before plating. After vortexing briefly, about 200ul of cells are plated on an LB-Tet plate (containing 10ug/ml of tetracycline). For the lacZ control insert, about 200ul of cells are added to the plate. Then

25     30ul of X-gal is added to the middle of the cells and the cells are immediately spread onto the LB-Tet plate. Unplated cells can be stored at 4°C if replating is needed within 1 week. Once the plate surface is dry, the plate is incubated upside-down overnight at 37°C. The

Tet colonies are scored and the plate is save upside-down at 4°C. Three individual Tet resistant colonies are picked for each clone with a 10ul pipette tip, placed in labeled sterile culture tube containing 3ml of LB broth and grown overnight at 37°C.

5      8. Screening colonies for inserts

Plasmid DNA was isolated using the Qiagen Qiaprep Miniprep kit. PCR was used to check for inserts in the plasmids. For each colony the following PCR reaction mixture was set up:

	dH2O	10μl
10	10xPCR buffer	2μl
	dNTPs (250μM)	1.6μl
	Left primer	2μl
	Right primer	2μl
	Plasmid DNA	2μl
15	Taq DNA Polymerase	0.2μl

The PCR parameters were 94°C for 30 sec, 52°C for 40 sec, 72°C for 1 min for 30 cycles followed by 5 min extension at 72°C and a final incubation at 4°C. All 20μl of the PCR product was analyzed on a 1.5% agarose gel with ethidium bromide staining.

20      Once the positive colonies were identified, they were sequenced by standard methods well-known to a skilled artisan. The sequences were compared to known sequences to determine if the sequence was already known.

As indicated at the beginning of Example 7, either differential display or microarray techniques were used to further determine genes related to penicillin hypersensitivity.

25

9. Genes Identified

By gel electrophoresis, about 260 candidate genes were identified and about 220 were cloned and sequenced to identify genes that predict hypersensitivity to penicillin. A summary of the genes associated with penicillin hypersensitivity is summarized in Table 10. Several new genes were identified that did not match any sequence listing in GenBank.

5 Novel sequences which did not match any BLAST searches or GenBank searches are indicated in Table 10 under the "Identification" column as "no significant match to anything". Thus, provided herein are nucleic acids comprising said novel sequences and fragments thereof as well as amino acid sequences encoded therefrom and fragments thereof. Also provided are nucleic acids that hybridize to said novel sequences under

10 stringent conditions. Such stringent conditions include conditions of a hybridization reaction that allow nucleic acid duplexes to be distinguished based on their degree of mismatch. Means for adjusting the stringency of a hybridization reaction are well-known to those of skill in the art. See, for example, Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, Second Edition, Cold Spring Harbor Laboratory Press, 1989;

15 Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1996 and periodic updates; and Hames *et al.*, NUCLEIC ACID HYBRIDIZATION: A PRACTICAL APPROACH, IRL Press, Ltd., 1985. In general, conditions that increase stringency (*i.e.*, select for the formation of more closely-matched duplexes) include higher temperature, lower ionic strength and absence of solvents; lower stringency is favored by lower

20 temperature, higher ionic strength, and higher concentrations of solvents (for example, formamide or dimethyl sulfoxide).

The following are some of the genes identified using the methods disclosed herein (GenBank identification numbers in parenthesis): hypothetical protein (HSPC004), UBA3 (UBA3) mRNA, clone CTA-732E4 on chromosome 22q12.1, ribosomal protein S7 (RPS7),  
25 myosin-binding protein C, cardiac (MYBPC3), CGI-51 protein mRNA, latexin mRNA, NADH oxidoreductase subunit MWFE, jun B proto-oncogene (JUNB), KIAA0787 protein, fatty acid synthase, polymerase (RNA) II (DNA directed) polypeptide B (140 kD), UbA52

gene coding for ubiquitin-52 amino acid fusion protein, small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) (SNRP70), isocitrate dehydrogenase 3 (NAD<sup>+</sup>) gamma (IDH3G), clone 565E6 on chromosome 11q12-1q22.2, hypothetical protein FLJ20436 (FLJ20436), c-Cbl-interacting protein L7a (RPL7A), ribosomal protein L7a (RPL7A),  
5 ribosomal protein S21 (RPS21), sorting nexin 6 (SNX6), TNF-inducible protein CG12-1 (CG12-1), BRCA2 gene region chromosome 13q12-13, CGI-128 protein mRNA, Tu translation elongation factor, mitochondrial (TUFM), KIAA0787 protein, ribosomal protein L13 (RPL13), ribosomal protein L19 (RPL19), clone 245M18 on chromosome 6p21.32-22.3, clone TCBA00781, chromosome 19 cosmid R26529, tumor suppressing  
10 subtransferable candidate 1 (TSSC1), transferrin receptor (TFRC), ubiquitin-conjugating enzyme E2D 3 (UBE2D3), putative DNA-directed RNA polymerase III C11 subunit, myosin-binding protein C (cardiac) (MYBPC3), tapasin (NGS-17), CoREST protein (COREST) (KIAA0071 protein), dynamin (dynactin complex 50 kD subunit) (DCTN-50), alpa-L-fucosidase, metallothionein-IG (MT1G), Familial Cylindromatosis cyld gene,  
15 cDNA FLJ10589 fis (clone NT2RP2004389), eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), chromosome 16 BAC clone CIT987SK-A-67A1, proteasome (prosome, macropain) subunit beta type 8 (large multifunctional protease 7) (PSMB8), and lectin galactoside-binding soluble 9 (galectin 9). An unexpected result that was found was that there were apparently no p450 genes or  
20 metabolism genes that were gene candidates for penicillin hypersensitivity.

#### 10. Gene Correlations

Gene expression profiles comprised of 180 genes on the penicillin array were compared for similarity between six penicillin-normal individuals and six self-identified penicillin-sensitive individuals. Three of the penicillin-sensitive profiles were repeat samples taken at different times. As shown in Figure 6, Samples 6005, 6015, and 6042 are from one individual, and samples 6041 and 6043 are from another individual. Using all genes for  
25

comparison, sensitive individuals tend to resemble one another while non-sensitive individuals have little discernable pattern. The one exception is non-sensitive individual 6002, whose profile has some resemblance to the sensitive individuals.

In an exploratory analysis, independent-samples t-tests were performed to suggest which genes were differentially expressed between penicillin-sensitive and penicillin-insensitive individuals. Twenty genes in which the p-value of the t-test showed a statistically significant difference between the two classes at a level of 0.005 or less were identified as indicated in Table 11. Using the 20 genes identified as "discriminator" genes, the correlation between normal individuals and the discriminator genes were calculated as well as the correlation between sensitive individuals and the discriminator genes. The discriminator correlations are shown in Figure 7. Using the 20 discriminator genes and relevance network grouping, a similar correlation resulted. At a 0.9 correlation level, the only group that reveals itself is among the sensitive individuals. At a lower similarity level of 0.8, non-sensitive individual #2, who appeared to be borderline hypersensitive, joins the group of sensitive individuals. Methods of analyzing expression data statistically which are known in the art may be used, such as those described in "Family-Wise Error Rate", Glass, G. and Hopkins, K., Statistical Methods in Education and Psychology (1984), Prentice-Hall; and "Relevance Networks", Butte, A. J. and Kohane, I. S. (2000), Mutual Information Relevance Networks: Functional Genomic Clustering Using Pairwise Entropy Measurements. PSB00, 5:415-426.

Figure 8 shows that the 20 discriminator genes were analyzed for co-regulation, revealing several co-varying groups, as shown in both the similarity matrix and the relevance network grouping.

25 10. Preparation of penicillin arrays

In addition to differential display, microarray techniques were utilized to determine genes related to penicillin hypersensitivity. The following are methods that were used to

prepare microarray for testing for penicillin hypersensitivity. Of 260 potential gel band, 220 were cloned and sequenced. About 180 genes were put on a penicillin array, made as described below, and 20 discriminator genes (Table 11) were selected related to penicillin hypersensitivity.

5

Large Scale PCR (in 96-well plates)

For 1000 PCR reactions, 4X Master Mix can be made with the following materials:

10

10X PCR buffer	10 ml
dATP	200ul (100mM)
dGTP	200ul (100mM)
dCTP	200ul (100mM)
15 dTTP	200ul (100mM)
Amine-linked vector primer (= "3X")	900ul (Forward or Reverse) 1ug/ml
Taq Polymerase	1 ml 5U/ml
H <sub>2</sub> O	<u>12.3 ml</u>
	<u>25 ml total</u>

20

About 2.5ml aliquots are put into 15ml conical tubes and store at -20°C. One tube is enough for 1 96-well plate of PCR. Alternatively, about 12.5ml aliquots can be used in 50ml conical tubes, which is enough for 5 plates of PCR. dNTPs was obtained from Pharmacia Ultrapure dNTP set, cat#27-2035-02 (set contains all 4, 1ml each) and Taq Polymerase was obtained from Perkin Elmer N808-0155 (comes with 10X buffer). Template and gene-specific primer mix was made for 2 rows, or 16 wells by utilizing the following materials: 400ul H<sub>2</sub>O, 2.5ul plasmid, 15ul of 1ug/ml gene specific primer.

25

To perform PCR, the following steps were performed:

30

1. Take one tube of PCR master mix and add 2 volumes of water (i.e., add 5ml water to 2.5ml MM).
2. Using a multichannel pipette, distribute 75ul MM to each well of a 96-well plate.
3. Add 25ul H<sub>2</sub>O to 2 wells of the plate to serve as negative controls.
4. Add 25ul template and gene-specific primer mix to appropriate wells.

- 5        5. Seal all wells with strip caps.
6. Plates can be stored at 4°C for up to 48 hours (maybe more) before cycling.
7. Run PCR using program TKB (95° for 5min, 95° for 15s, 50° for 30s, 72° for 30s, go to step of 95° for 15s and repeat 34 times, 72° for 10min., 4° until PCR needed for subsequent steps
8. Run product on 1.5% agarose gel and check insert size. (Only need to check 1 well of each "gene.")
9. Clean PCR products using any commercially available kit for cleaning PCR products.

10

#### Gene purification

The ArrayIt™ kit from TeleChem, International, Inc. Sunnyvale, CA was used for gene purification. The following protocol was used:

- 15        1. Position a SuperFilter 100 on a 96-well vacuum manifold. Make sure the SuperFilter is properly fitted to allow a tight seal for vacuum filtration.
2. Add 500 µl of ArrayIt™ Binding Buffer to each well of the SuperFilter 100 using a 12-channel pipetting device set for 500 µl. Pipetting should be performed as quickly as possible (within 1 minute per plate) to minimize the loss of the Binding Buffer due to gravity flow. Avoid splashing the contents from well to well.
- 20        3. Quickly add 100 µl per well of PCR sample for a 96-well plate to the corresponding well of the SuperFilter 100. Transfer the PCR samples to the SuperFilter 100 as quickly as possible (within 1 minute per plate) to minimize the loss of the Binding Buffer due to gravity flow.
- 25        4. Immediately mix the Binding Buffer and the PCR sample thoroughly by pipetting up and down 10 times with an automatic pipetting device. Mixing should be completed as quickly as possible (within 5 minutes after adding the Binding Buffer to the SuperFilter

- 100) to minimize the loss of the Binding Buffer due to gravity flow. void splashing the contents from well to well.
5. Apply a gentle vacuum such that a little trickle flows from the SuperFilter 100 to allowing binding of the PCR product to the SuperFilter 100 membrane. Primers, nucleotides, single-stranded products, salts, and other impurities pass through the SuperFilter 100 into the waste reservoir at the bottom of the vacuum filtration block.
- 10 6. Shut off the vacuum and add 800 µl of Wash Buffer to eachwell of the SuperFilter 100 with a 12-channel pipetting device. Apply a gentle vacuum until all of the Wash Buffer has passed through the SuperFilter 100 membrane. The 800 µl of Wash Buffer used in the first wash step is necessary to remove Binding Buffer and PCR sample that adheres to the walls of the SuperFilter 100 during mixing.
- 15 7. Shut off the vacuum and add 100 µl per well of Wash Buffer to the SuperFilter 100 with a 12-channel pipetting device. Apply a gentle vacuum until all of the Wash Buffer has passed through the membrane. Repeat this step with an additional 100 µl of Wash Buffer. The second and third wash steps remove additional trace contaminants from the bound PCR Product.
- 20 8. Apply a full vacuum for 3 minutes to dry the SuperFilter membrane. This removes small amounts of Wash Buffer that may interfere with the elution step and assists in fixing the DNA to the filter prior to elution.
9. Remove the SuperFilter 100 from the vacuum manifold and place it on an unmarked 96-well microplate.
- 25 10. Centrifuge the two plates for 5 minutes at ambient temperature in a microplate centrifuge (~500xg) to remove trace amounts of Wash Buffer. This step aids in eluting the DNA from the SuperFilter and improves yield.
11. Discard the unmarked microplate containing the residual wash Buffer.
12. Transfer the SuperFilter 100 containing the bound PCR product onto a marked 96-well microplate.

13. Re-hydrate the ArrayIt™ SuperFilter by adding 75 µl per well of H<sub>2</sub>O (pH=8.0) with an automatic pipetting device. For maximal DNA recovery, be sure to add the 0.1X TE directly onto the surface of the SuperFilter membrane. The mild elution buffer (1mM TrisCl, 0.1 mM EDTA) is used to minimize the interference of the buffer in downstream applications.

Attaching hypersensitivity relevant genes to glass slide

The genes to be attached to the glass slides are amplified as provided herein. An important modification to the amplification process is the inclusion of amine primers, which can be obtained from any commercial source, i.e. Synthegen, such that a reactive amine group, a derivative thereof, or another reactive group is included in the amplified product. The amplified product is purified by any number of methods disclosed herein and immobilized or "spotted" onto a solid substrate, such as a glass slide, which can react with the amine group on the amplified product and form a covalent linkage.

An MD Generation II Array Spotter main instrument (Molecular Dynamics, 928 East Arques Avenue, Sunnyvale CA 04-86-4520) was used for spotting the hypersensitive genes according to following parameters:

MD ARRAY SPOTTER OPERATION

20	The terminology and equipment used in this example comprised the following:
	Spotter: MD Generation II Array Spotter main instrument
	Spotting Chamber: Area of spotter enclosed in glass which houses the pins, plates, trays and most spotter machinery.
25	Controller: Dedicated Dell Computer and Monitor to right of Spotter Unit
	Pins: (6) fine tubes in the Spotter Unit which pick-up and spot the Target
	Slides: Std. size glass microscope slides with a special coating on one side
	Plates: Plastic 96 well plates which hold the Target solution to be spotted
	Target: A solution of PCR product which the spotter deposits on the slides.
30	N2 Tank: 5 ft. high steel gas tank labeled "Nitrogen, Compressed"
	N2 : The N2 gas from the N2 tank
	Air Conditioner: Kenmore air conditioner installed in window of spotting chamber
	Humidifier 1: Essick 2000 Evaporative Cooler against the window

	Humidifier 2:	Bemis Airflow with white flexible duck into the Spotter Unit
	Humidifier 3:	Bemis Airflow against the wall
	Humidifier 4:	Kenmore QuietComfort 7
	Vacuum Pump:	Gast Laboratory Oilless Piston Vacuum Pump
5	Dampbox:	The plastic sealable container containing an NaCl / water slurry

Materials used for reagent solutions are: Nanopure water, 0.2 M KCl (1/10 dilution of Stock 2M KCL in water), and 95% EtOH Reagent. The temperature control is adjusted to 60°. The spotter chambers are adjusted to be greater than 39 % relative humidity and  
10 less than 65° C. The spotting pins are pre-washed for 20 cycles.

Slide Preparation/Loading:

When the pre-wash is completed, the slides are first each blown with N<sub>2</sub> gas for about 2 seconds per side. The slides are inserted into the Spotter following Array Spotter  
15 Run Values. The slides are aligned using a clean narrow rod orienting it on the center right edge of the slide and gently pushed to the left until the slide is aligned vertically against the metal pins. After slides are loaded and straightened, a visual check is done to make sure no more debris had fallen. The humidity is confirmed to be greater than 39% relative  
humidity. The MD spotter recognizes 16 plates as a maximum for a run and will pause  
20 automatically after 8 plates. The MD spotter also advances sequentially to plates in an invariable order and is not programmable to accommodate unique plate sourcing scheme. Therefore, it is important to manually rotate (or shuffle) plates to accomplish the spotting for the canine arrays.

25 Blocking (Slide Preparation post-spotting)

This blocking procedure is important because it reduces the non-specific background signals. The amounts provided in this protocol are for 19 slides, however, a skilled artisan may make modifications accordingly. More staining dishes and slide racks will be required if more than 19 slides are to be blocked. A clean glass container is obtained

and filled with Nanopure H<sub>2</sub>O. The container is placed on a hot plate and heated to a high temperature. A blocking solution is made by adding 2.5 ml of 20% SDS to 500mL blocking solution bottle. The blocking solution is warmed in microwave for 2.5 minutes and checked to determine if the temperature had reached 50°C. If the temperature of the  
5 solution is not at yet 50°C, then the solution is warmed in the microwave at 10 second intervals until it reached the desired temperature. One staining dish is placed on an orbital shaker with 4x SSC solution and turned to an agitation speed of 75 rpm. Slides are placed in metal racks and placed in boiling water for several minutes (i.e. 2 minutes). The slides are taken out of boiling water and allowed to cool briefly. The slides are then transferred to  
10 staining container containing 4x SSC solution on orbital shaker for several minutes (i.e. 2 minutes), rinsed with nanopure water in a staining container, and then briefly placed in blocking solution for about 15 minutes. After 15 minutes, the slides are taken out of the blocking solution and rinsed three times by dipping into three separate containers with nanopure water each time. The tops of the slides are dabbed lightly with a tissue and the  
15 slides are placed in a centrifuge for about 5 minutes at a speed of 1000 rpm.

#### Microarray RT Reaction

An exemplary procedure for labeling the probes is as follows. Fluorescence-labeled first strand cDNA probe is made from total or mRNA by first isolating RNA from control  
20 and treated cells, disclosed *supra*. This probe is hybridized to microarray slides spotted with DNA specific for hypersensitivity relevant genes. The materials needed to practice this example are: total or messenger RNA, primer, Superscript II buffer, dithiothreitol (DTT), nucleotide mix, Cy3 or Cy5 dye, Superscript II (RT), ammonium acetate, 70% EtOH, PCR machine, and ice.

25 The volume of each sample that would contain 20µg of total RNA (or 2µg of mRNA) is calculated. The amount of DEPC water needed to bring the total volume of each RNA sample to 14 µl is also calculated. If RNA is too dilute, the samples are concentrated

to a volume of less than 14  $\mu$ l in a speedvac without heat. The speedvac must be capable of generating a vacuum of 0 Milli-Torr so that samples can freeze dry under these conditions. Sufficient volume of DEPC water is added to bring the total volume of each RNA sample to 14  $\mu$ l. Each PCR tube is labeled with the name of the sample or control reaction. The appropriate volume of DEPC water and 8  $\mu$ l of anchored oligo dT mix (stored at -20°C) is added to each tube.

Then the appropriate volume of each RNA sample is added to the labeled PCR tube. The samples are mixed by pipeting. The tubes are kept on ice until all samples are ready for the next step. It is preferable for the tubes to kept on ice until the next step is ready to proceed. The samples are incubated in a PCR machine for 10 minutes at 70°C followed by 4°C incubation period until the sample tubes are ready to be retrieved. The sample tubes are left at 4°C for at least 2 minutes.

The Cy dyes are light sensitive, so any solutions or samples containing Cy-dyes should be kept out of light as much as possible (i.e. cover with foil) after this point in the process. Sufficient amounts of Cy3 and Cy5 reverse transcription mix are prepared for one to two more reactions than would actually be run by scaling up the following protocols:

For labeling with Cy3

8 ul 5x First Strand Buffer for Superscript II  
4 ul 0.1 M DTT  
20 2 ul Nucleotide Mix  
2 ul of 1:8 dilution of Cy3 (i.e., 0.125mM Cy3 dCTP).  
2 ul Superscript II

For labeling with Cy5

8 ul 5x First Strand Buffer for Superscript II  
25 4 ul 0.1 M DTT  
2 ul Nucleotide Mix  
2 ul of 1:10 dilution of Cy5 (i.e., 0.1mM Cy5 dCTP).  
2 ul Superscript II

About 18  $\mu$ l of the pink Cy3 mix is added to each treated sample and 18  $\mu$ l of the blue Cy5 mix is added to each control sample. Each sample is mixed by pipeting. The samples are placed in a PCR machine for 2 hours at 45°C followed by 4°C until the sample

tubes are ready to be retrieved. The samples are transferred to Eppendorf tubes containing 600  $\mu$ l of ethanol precipitation mixture. Some of the EtOH precipitation mixture is used to rinse the PCR tubes. The tubes are inverted to mix. Samples are placed in -80°C freezer for at least 20-30 minutes. If desired, samples may be left at -20°C overnight or over the

5 weekend.

The samples are centrifuged for 15 minutes at 20800 x g (14000 rpm in Eppendorf model 5417C) and carefully the supernatant is decanted. A visible pellet is seen (pink/red for Cy3, blue for Cy5). It is preferable to centrifuge the tubes at a fixed position so the pellet will be at a known area in the tube. In some rare instances, the probe is seen spread 10 on one side of the tube instead of a tight pellet. If the pellet is white or nonexistent, the reaction has not occurred to maximal efficiency.

Ice cold 70% EtOH (about 1 ml per tube) is used to wash the tubes and the tubes are subsequently inverted to clean tube and pellet. The tubes are centrifuged for 10 minutes at 20800 x g (14000 rpm in Eppendorf model 5417C), then the supernatant is carefully 15 decanted. The tubes are flash spun and any remaining EtOH is removed with a pipet. The tubes are air dried for about 5 to 10 minutes. protected from light. The length of drying time will depend on the natural humidity of the environment. For example, an environment in Santa Fe would require about 2 to 5 minutes of drying time. It is preferable that the pellet are not overdried.

20 When the pellets are dried, they are resuspended in 80  $\mu$ l nanopure water. The cDNA/mRNA hybrid is denatured by heating for 5 minutes at 95°C in a heat block and flash spun.

To purify fluorescence-labeled first strand cDNA probes, the following materials are used: Millipore MAHV N45 96 well plate, v-bottom 96 well plate (Costar), Wizard 25 DNA binding Resin, wide orifice pipette tips for 200 to 300  $\mu$ l volumes, isopropanol, nanopure water. It is highly preferable to keep the plates aligned at all times during

centrifugation. Misaligned plates lead to sample cross contamination and/or sample loss. It is also important that plate carriers are seated properly in the centrifuge rotor.

The lid of a "Millipore MAHV N45" 96 well plate is labeled with the appropriate sample numbers. A blue gasket and waste plate (v-bottom 96 well) is attached. Wizard DNA Binding Resin (Promega cat#A1151) is shaken immediately prior to use for thorough resuspension. About 160 µl of Wizard DNA Binding Resin is added to each well of the filter plate that is used. If this is done with a multi-channel pipette, wide orifice pipette tips would have been used to prevent clogging. It is highly preferable not to touch or puncture the membrane of the filter plate with a pipette tip. Probes are added to the appropriate wells (80 µl cDNA samples) containing the Binding Resin. The reaction is mixed by pipeting up and down ~10 times. It is preferable to use regular, unfiltered pipette tips for this step. The plates are centrifuged at 2500 rpm for 5 minutes (Beckman GS-6 or equivalent) and then the filtrate is decanted. About 200 µl of 80% isopropanol is added, the plates are spun for 5 minutes at 2500 rpm, and the filtrate is discarded. Then the 80% isopropanol wash and spin step is repeated. The filter plate is placed on a clean collection plate (v-bottom 96 well) and 80 µl of Nanopure water, pH 8.0-8.5 is added. The pH is adjusted with NaOH. The filter plate is secured to the collection plate with tape to ensure that the plate did not slide during the final spin. The plate sat for 5 minutes and is centrifuged for 7 minutes at 2500 rpm. If there are replicates of samples they should be pooled.

To semi-quantitatively assess the incorporation of fluorescence into cDNA probes and to concentrate probes prior to hybridization, the following material is used: 384 well, 100 µl assay plate (Falcon Microtest cat#35-3980) and Wallac Victor 1420 Multilabel counter (or equivalent).

It is preferable that a consistent amount of cDNA is pipeted into the 384-well plate wells because readings will vary with volume. Controls or identical samples should be pooled at this step, if required. The probes are transferred from the Millipore 96 well plate to every other well of a 384 well assay plate (Falcon Microtest). This is done using a multi-

channel pipette. For replicate samples that have been pooled, 60  $\mu$ l aliquots are transferred into wells of the assay plate.

The Cy-3 and Cy-5 fluorescence is analyzed using the Wallac 1420 workstation programmed for reading Cy3-Cy-5 in the 384-well format and the data is saved to disk.

- 5      The typical range for Cy-3 (20 $\mu$ g) is 250-700,000 fluorescence units. The typical range for Cy-5 (20 $\mu$ g) is 100-250,000 fluorescence units. Settings for the Wallac 1420 fluorescence analyzer are as follows:

Cy3

10     CW lamp energy        = 30445  
Lamp filter                = P550 slot B3  
Emission filter= D572 dysprosium slot A4  
Emission aperture        = normal  
Count time                = 0.1 s

15     Cy5

20     CW lamp energy        = 30445  
Lamp filter                = D642 samarium slot B7  
Emission filter= D670 slot A8  
Emission aperture        = normal  
Count time                = 0.1 s

The dry-down process of the probes is as follows. Concentration of the cDNA probes is highly preferable so that they can be resuspended in hybridization buffer at the appropriate volume. The volume of the control cDNA (Cy-5) is measured and divide by the number of samples to determine the appropriate amount to add to each test cDNA (Cy-3).

- 25     Eppendorf tubes are labeled for each test sample and the appropriate amount of control cDNA is allocated into each tube. The test samples (Cy-3) are added to the appropriate tubes. These tubes are placed in a speed-vac to dry down, with foil covering any windows on the speed vac. At this point, heat (45°C) may be used to expedite the drying process. Time will vary depending on the machinery. The drying process takes about one hour for
- 30     150  $\mu$ l samples dried in the Savant. Samples may be saved in dried form at -20°C for up to 14 days.

To hybridize labeled cDNA probes to single stranded, covalently bound DNA target genes on glass slide microarrays, the following material are used: formamide, SSC, SDS, 2  $\mu$ m syringe filter, salmon sperm DNA, hybridization chambers, incubator, coverslips, parafilm, heat blocks. It is preferable that the array is completely covered to ensure proper hybridization.

About 30  $\mu$ l of hybridization buffer is prepared per sample. Slightly more than is what is needed should be made since about 100  $\mu$ l can be lost during filtration.

	<u>Hybridization Buffer:</u>	<u>for 100 <math>\mu</math>l:</u>
10	• 50% Formamide	50 $\mu$ l formamide
	• 5X SSC	25 $\mu$ l 20X SSC
	• 0.1% SDS	25 $\mu$ l 0.4% SDS

The solution is filtered through 0.2  $\mu$ m syringe filter, then the volume is measured.

15 About 1  $\mu$ l of salmon sperm DNA (10mg/ml) is added per 100  $\mu$ l of buffer. Materials used for hybridization are: 2 Eppendorf tube racks, hybridization chambers (2 arrays per chamber), slides, coverslips, and parafilm. About 30  $\mu$ l of nanopure water is added to each hybridization chamber. Slides and coverslips are cleaned using N<sub>2</sub> stream. About 30  $\mu$ l of hybridization buffer is added to dried probe and vortexed gently for 5 seconds. The probe remained in the dark for 10-15 minutes at room temperature and then is gently vortexed for several seconds and then is flash spun in the microfuge. The probes are boiled for 5 minutes and centrifuged for 3 min at 20800 x g (14000 rpm, Eppendorf model 5417C). Probes are placed in 70 °C heat block. Each probe remained in this heat block until it is ready for hybridization.

20 25 Pipette 25  $\mu$ l onto a coverslip. It is highly preferable to avoid the material at the bottom of the tube and to avoid generating air bubbles. This may mean leaving about 1  $\mu$ l remaining in the pipette tip . The slide is gently lowered, face side down, onto the sample so that the coverslip covered that portion of the slide containing the array. Slides are

placed in a hybridization chamber (2 per chamber). The lid of the chamber is wrapped with parafilm and the slides are placed in a 42°C humidity chamber in a 42°C incubator . It is preferable to not let probes or slides sit at room temperature for long periods. The slides are incubated for 18-24 hours.

5 To obtain single stranded cDNA probes on the array, all non-specifically bound cDNA probe should be removed from the array. Removal of all non-specifically bound cDNA probe is accomplished by washing the array and using the following materials: slide holder, glass washing dish, SSC, SDS, and nanopure water. It is highly preferable that great caution be used with the standard wash conditions as deviations can greatly affect  
10 data.

Six glass buffer chambers and glass slide holders are set up with 2X SSC buffer heated to 30-34°C and used to fill up glass dish to 3/4th of volume or enough to submerge the microarrays. It is important to exercise caution in heating of the 2X SSC buffer since a temperature of greater than 35°C might strip off the probes. The slides are removed from  
15 chamber and placed in glass slide holders. It is preferable that the slides are not allowed dry out. The slides are placed in 2X SSC buffer but it is recommended that no more than 4 slides be placed per dish. Coverslips should fall off within 2 to 4 minutes. In the event that the coverslips do not fall off within 2 to 4 minutes, very gentle agitation may be administered. The stainless steel slide carriers are placed in the second dish and filled with  
20 2X SSC, 0.1%SDS. Then the slides are removed from glass slide holders and placed in the stainless steel holders submerged in 2X SSC, 0.1%SDS and soaked for 5 minutes. The slides are transferred in the stainless steel slide carrier into the next glass dish containing 0.1X SSC and 0.1%SDS for 5 minutes. Then the slides are transferred in the stainless steel carrier to the next glass dish containing only 0.1X SSC for 5 minutes. The slides, still in  
25 the slide carrier, is transferred into nanopure water (18 megaohms) for 1 minute.

To dry the slides, the stainless steel slide carriers are placed on micro-carrier plates with a folded paper towel underneath. The top of the slides are gently dabbed with a tissue.

Then the slides are spun in a centrifuge (Beckman GS-6 or equivalent) for 5 minutes at 1000 rpm. It is very important that the slides do not air dry, as this will lead to increased background.

When the examples are practiced by a skilled artisan as disclosed, an analysis of a  
5 toxicological response to an agent, for example, cadmium chloride, can be obtained.

#### Preparation of cDNA

The following materials were used to prepare cDNA from RNA: total or messenger RNA; 3DNA™ Submicro™ Expression Array Detection Kit (Genisphere 3DNA 14  
10 Phillips Parkway Montvale, NJ 07645; Kit numbers: K20F00-41 and K20F00-31); Linear Acrylamide (Ambion); RNase free water (Ambion); 0.5M NaOH/50mM EDTA; 1M Tris-HCl, pH 7.5; 10mM Tris pH 8/1mM EDTA; 3M Ammonium Acetate; 70% Ethanol (Aldrich); 100% Ethanol (Aldrich); Denhardt's Salmon Sperm DNA (Sigma); RNase Zap (Ambion); Thermal Cycler; -80°C Freezer; Heat block; 4°C Microfuge; SpeedVac;  
15 MicroArray slides; Coverslips; Hybridization Chamber; 42°C Humidity Chamber; Parafilm.

For synthesis of cDNA, prepare 2 separate identical reactions for each sample. In a PCR or 1.5ml tube combine: 1.5ug lymphocyte RNA in 7ul DEPC treated water (if sample is too dilute, concentrate it in the SpeedVac at room temperature), and 3ul RT Primer.  
20 Separate tubes for treated and untreated RNA. Heat mixture to 80°C for 10 minutes, 4°C for 2 minutes. Place samples on ice and add the following: 4ul 5X RT buffer, 1ul dNTP mix, 4ul RNase free water, and 1ul Reverse transcriptase enzyme. Gently mix and centrifuge the contents of the tube. Incubate at 42°C for 1.5 to 2 hours. Stop the reaction by adding 3.5ul of 0.5M NaOH/50nM EDTA. Incubate at 65°C for 10 minutes to denature  
25 the DNA/RNA hybrids. Neutralize the reaction with 5ul of 1M Tris-HCL, pH 7.5. Transfer to 1.5ml tube if in PCR tube and add 38.5ul of 10mM Tris, pH8/1mM EDTA. Precipitate by adding the following to each tube: 4ul Linear acrylamide, 175ul 3M

Ammonium Acetate, and 625 $\mu$ l 100% Ethanol. Incubate at -80°C for 30 minutes. Centrifuge at 13,000 rpm in 4°C centrifuge for 15 minutes. Carefully decant supernatant.

### 11. Taqman® RT Reaction

5       Taqman® technology from Roche Molecular System was used in the following manner. The mRNA was converted to cDNA using 3 $\mu$ g total RNA and 1.5 $\mu$ l random hexamer primers. After a 10 minute incubation at 70°C the following components were added to the reaction mixture: 6 $\mu$ l of 5x first strand buffer, 3 $\mu$ l 0.1 DTT, 1.5 $\mu$ l 10mM dNTPs, 1.5 $\mu$ l Superscript enzyme and 6.5 $\mu$ l DEPC-treated water. The reaction is  
10      incubated for two hours at 45°C and 1 $\mu$ l of this reaction is used for the Taqman® assay. For the Taqman® assay 50 $\mu$ l reactions were set up with Rnase-free water, Taqman® Universal PCR Master Mix, target and control primers /probes and cDNA.

15      Real time PCR can be performed using the Taqman® assay . The method measures PCR product accumulation with a dual-labeled fluorogenic probe. The probes are labeled with 6-FAM on the 5' end and TAMRA on the 3' end. TAMRA is a quencher dye. This assay exploits the 5'-3' exonuclease property of Taq polymerase. When the probe hybridizes to its target the reporter dye (FAM) is cleaved by the 5' exonuclease activity of the Taq polymerase and can emit a fluorescent signal. With increasing cycles of amplification more signal is emitted and detected using an ABI 7700 sequence detector.  
20      For each gene, a set of two primers and a fluorogenic probe are designed and synthesized. For quantitation of mRNA the best design for probes and primers requires primers to be positioned over exon-intron junctions. This rules out amplification of contaminating genomic DNA. For initial studies, primer and probe sets have been designed for 13 genes that were up- or down-regulated by penicillin in differential display experiments. The  
25      probes and primer sets were tested for their ability to amplify genomic DNA. If genomic DNA was amplified, the probes and primers for that particular gene were not used for the Taqman® assay. Figure 9 and 10 show results obtained with a penicillin sensitive person

as well as a penicillin refractive person. The genes in these figures are as follows: 1A is Inhibitor of apoptosis protein-1, 76B is cyclin D2, 142B is Fc-gamma-receptorIIA (FCGR2A), 167B is chromosome 16 clone, RP11-296I10 198A is ribosomal protein S24 (RPS24a), 198B is ribosomal protein S24 (RPS24a). The Y-axis refers to levels of gene expression based on ABI Prism 7700 Realitive Quantification Software, in which cDNA levels are measured based on Ct (Cycle Threshold) values between control and treated samples.

5           Example8: Differential Protein Expression in Penicillin Treated and Untreated Human  
10          Lymphocytes from Penicillin Sensitive and Refractive Individuals

Protein expression in lymphocytes was studied using two technologies, SDS Polyacrylamide Electrophoresis (SDS-PAGE) and Surface Enhanced Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (SELDI-TOF) of proteins applied to ProteinChips. Differences in protein profiles, treated and untreated, for sensitive and refractive samples were observed using both techniques. The following methods were used:

15          Cell Preparation

For these experiments, blood was drawn from four refractive (control) individuals and two penicillin-sensitive individuals. White blood cells were isolated and cultured for 20 hours, using standard cell culture conditions. The cultures were split, half the cells were treated with penicillin, and all cells were grown for an additional 24 hours. Media was removed by centrifugation. Cells were then subjected to hypotonic lysis in nanopure water, followed by centrifugation to remove solid cellular debris. The supernatants were frozen prior to protein experiments. Cell lysates were concentrated by vacuum centrifugation 25 prior to SDS-PAGE and ProteinChip experiments.

SDS-PAGE

Proteins were electrophoresed using a Bio-Rad MiniProtean gel apparatus, on ReadyGel Precast 4-20% acrylamide gels, using the standard method of Laemmli. For each concentrated lysate, 20 ul sample was mixed with 5 ul 5X SDS sample buffer. The samples were boiled for 10 minutes in the presence of 2-mercaptoethanol and half of each sample was loaded into corresponding wells on two identical gels. Two stains were used to visualize proteins in the replicate gels, Coomassie Blue and Ruby SYPRO (BioRad).  
5 Bands were observed directly for Coomassie stained gels, and by fluorescence scanning (Hitachi Scanner) for Ruby stained gels. All gels were dried in cellophane membranes as permanent records stored in (the laboratory notebook).

10

#### ProteinChip/SELDI-TOF

ProteinChips were obtained from Ciphergen Biosystems. Chips containing spots with hydrophobic (H4) and normal phase (NP) chromatographic surfaces were used. For the H4 surface, 1 ul acetonitrile was pipetted onto each spot to pre-wet the C-18 surface.  
15 Nanopure water was used to wet the normal phase chip. Three microliters of concentrated lysate was added to each spot on replicate chips, with eight spots/samples per chip. The spots were dried at room temperature, then washed with 10% acetonitrile and nanopure water, for the H4 and NP chips, respectively. Washes were performed by pipetting 5 ul wash solution onto each spot, allowing a 5 minute incubation to resolubilize  
20 non-specifically bound biomolecules, and pipetting in and out five times prior to removing the wash buffer. Spots were dried under a 100 Watt bulb (placed 2 feet above benchtop). Each spot was then treated with 0.5 ul sinapinic acid (saturated in 50% acetonitrile, 0.5% trifluoroacetic acid), which acts as an energy absorbing "matrix" to assist laser ionization of proteins. Proteins were detected directly from the chips using a PBS-II mass spectrometer  
25 (Ciphergen Biosystems). Spectra were electronically stored in powerpoint files.

#### Results

Using both techniques, differences were observed in the protein profiles of treated and untreated, sensitive and refractive samples. The SDS-PAGE 1-D data is low resolution, but clearly shows increased production of at least four proteins in penicillin-treated sensitive cells, compared with the controls. Sensitivity was comparable for SELDI-  
5 TOF on ProteinChips is a more sensitive technique, and showed hundreds of peaks in each profile. The differences in protein spectra were striking, showing that refractive cells exhibit protein induction that is different than the induction in sensitive cells. While many differences were observed (at least 5-10 proteins), the similarities in the overall profiles  
10 was striking, and permits reasonable difference comparison by providing internal standards.

TABLE 1

<b>Generic Name</b>
acetaminophen
acetaminophen/codeine
acetohydroxamic acid
actinomycin D
acyclovir
adenosine
albuterol
alendronate
alendronate sodium
alglucerase
allopurinol
alosetron
alprazolam
alprostadiol
alteplase
ambenonium
amifostine
amiloride
aminobenzoate potassium
aminoglutethimide
aminopurine
aminosalicylate sodium
amiodorone
amitriptyline
amlodipine
amoxapine
amoxicillin
amphetamine mixed salts
ampicillin
amprenavir
amyl nitrite
anagrelide
ancrod
androgens
anistreplase
anthralin
araC
aspirin
aspirin
astemizole
atenolol
atorvastatin

atovaquone
atropine
attapulgite
azathioprine
azelastine
azithromycin
aztreonam
bacampicillin
baclofen
beclomethasone
belladonna
benazepril
benazepril
benzodiazepines
benzoyl peroxide
benztropine
beta carotene
betamethasone
betamethasone
betamethasone valerate
bethanechol
bisacodyl
bismuth subsalicylate plus
bisoprolol/HCTZ
bleomycin
bradykinin antagonist
bromfenac
brominide tartrate
bromocriptine
bronchodilators
bucizine
budesonide
bumetanide
bupropion HCL
buspirone
busulfan
calcipotriene
calcitonin salmon
calfactant
candesartan cilexetil
capsaicin
captopril
carbamazapine
carbenicillin
carbidopa
carboplatin

carisoprodol
carmustine
carvedilol
cefaclor
cefepime
cefprozil
ceftibuten
cefuroxime
celecoxib
cephalexin
cephalosporins
cerivastatin
cetirizine
chenodiol
chllophedianol
chloral hydrate
chlorambucil
chloramphenicol
chloroquine
chlorpropamide
chlorthalidone
chlorzoxazone
cholestyramine
cimetidine
cinoxacin
ciprofloxacin
(+)-cis-3,5-dimethyl-2-(3-pyridyl)thiazolidin-4
cisapride
cisplatin
citalopram
clarithromycin
clavulanate
clavulanate
clavulanic acid
clidinium
clindamycin
clofibrate
clomiphene
clonazepam
clonidine
clotrimoxazole
cloxacillin
clozapine
codeine
colchicine

colestipol
collagen-alginate
conjugated estrogens
copolymer-1
cortisone
courmarin
cromolyn
cyclacillin
cyclandelate
cyclizine
cyclobenzaprine
cyclopegic
cyclopentolate
cyclophosphamide
cycloserine
cyclosporine
cyclosporine A
cytoxin
dalteparin injection
danazol
dantrolene
dapsone
daunomycin
daunorubicin
dehydrocholic acid
desmopressin
desogestrel
dexamethasome
dextromethorphan
dextrothyroxine
diazepam
diazoxon
dichloralphenazone
diclofenac
diclofenacdihydrazine
dicloxacillin
dicyclomine
didanosine
difenoxin
digitalis glycosides
digoxin
dihydrazine
dihydroergotamine mesylate
dihydrolazine
diltiazem
dimethyl sulfoxide

dinoprostone
dione
diphenidol
diphenoxylate
dipyridamole
dipyridamole
disopyramide
disulfiram
divalproex
divalproex sodium
docusate sodium
dolasetron mesylate
donepezil
doxazosin
doxercalciferol
doxorubicin
doxycycline
enalapril
enoxaparin
entacapone
ephedrine
epirubicin
eptifibatide
ergoloid mesylates
ergonovine
erythromycin
estradiol
estrامustine
etanercept
ethacrynic acid
ethchlorvynol
ethinamate
ethinyl estradiol
ethinyl estradiol
ethionamide
etidronate
etoposide
etretinate
exemestane
famciclovir
famotidine
felbamate
felodipine
felodipine SR
fenofibrate
fenoldopam mesylate

fentanyl citrate
fexofenadine
fialuridine
finasteride
flavoxate
flecainide acetate
flosequinan
fluconazole
flunisolide
fluoroquinolones
fluorouracil
fluoxetine
flutamide
fluticasone
fluticasone
fluticasone propionate
fluvastatin
fluvoxamine maleate
foscarnet sodium
fosinopril
fosphenytoin
furazolidone
furosemide
gabapentin
ganciclovir
ganirelix acetate
gemcitabine
gemfibrozil
glimepiride
glipizide
glucagon
glyburide
glycopyrrolate
gold compounds
gold sodium thiomalate
granisetron
grepafloxacin
griseofulvin
guaifenesin
guanabenz
guanadrel
guanethidine
guanfacine
haloperidol
heparin
hismanol

hydantoin
hydralazine
hydrochlorothiazide
hydrocodone
hydrocortisone
hydroxychloroquine
hydroxyurea
hydroxyzine
hyoscine
hyoscyamine
hyoscyamine
hyperozia
ibuprofen
ibutilide fumarate
imiglucerase injection
imiquimod 5% cream
inactivated hepatitis A vaccine
indapamide
indinavir
indomethacin
insulin
interferon-beta-1a (recombinant)
interferon-beta-1b (recombinant)
iodinated glycerol
iodoquinol
ippecac
iphosphamide
ipratropium
irbesartan
irinotecan
isomethptene
isoniazid
isoproterenol
isosorbide mononitrate S.A.
isotretinoin
isoxyprine
isradipine
itraconazole
kanamycin
ketoconazole
ketorolac
lactulose
lamivudine, 3TC
lamotrigine
lansoprazole
latamoxef

latanoprost
leflunomide
letrozole
leucovorin
leuprolide
levamisole
levetiracetam
levobupivacaine
levocabastine
levocarnitine
levodopa
levofloxacin
levonorgestrel
levothyroxine
lidocaine
lincomycin
liposomal amphotericin B
lisinopril
lispro insulin
lithium
I-norgestrel
I-norgestrel/ethinyl estradiol
lomustine
loperamide
loracarbef
loratadine
Loratadine/Pseudoephedrine
lorazepam
losartan
lovastatin
loxapine
magnesium sulfate
maprotiline
masoprocol
mazindol
mecamylamine
mechlorethamine
meclizine
medroxyprogesterone
medroxyprogesterone
mefloquine
melatonin
melphalan
menotropin
meprobamate
merbarone

mercaptopurine
meropenem
mesalamine
metformin
methenamine
methicillin
methotrexate
methylcellulose
methyldopa
methylergonovine
methylphenidate
methylprednisolone
methyprylon
methysergide
metoclopramide
metoprolol
metoprolol
metronidazole
metyrapone
metyrosine
mexiletine
mibepradil
miconazole cream 2%
milglitol
minocycline
minoxidil
misoprostol
misoprostol
mitotane
mixed amphetamines
moclobemide
molindone
mometasone
moricizine
moxifloxacin
mupirocin
nabilone
nabumetone
nafarelin
naftillin
nalidixic acid
naltrexone
naproxen
naratriptan
natamycin
navirapine

nedocromil
nefazodone
neomycin
Neomycin/Polymx/HC
neostigmine
nicardipine
nicorandil
nicotine
nifedipine
nimodipine
nitrofurantoin
nitroglycerin
nizatidine
norethindrone
norethindrone/ ethinyl estradiol
norgestimate
norgestimate/ethinyl estradiol
norgestrel
norgestrel/ethinyl estradiol
nylidrin
nystatin
ofloxacin
olsalazine
omeprazole
orphenadrine
oxacillin
oxaprozin
oxatriphylline
oxybutynin
oxycodone
oxymetazoline
paclitaxel
pancreatin
pancrelipase
papaverine
paraldehyde
paramethasone
paregoric
paroxetine
pediculicides
pemoline
penicillamine
penicillin
pentamidine
pentoxifylline
pepsin

pergolide
perhexiline
perindopril
perphenazine
pexiganan acetate
phenazopyridine
phendimetrazine
phenformin
phenobarbital
phenolphthalein
phenothiazines
phentermine
phenylephrine
phenylephrine
phenylpropanolamine
phenylpropanolamine
phenytoin
pilocarpine
pioglitazone
piroxicam
podophyllum
poloxamer 188
polycarbophil calcium
Polyethylene glycol
polythiazide
potassium chloride
potassium iodide
potassium phosphates
pramipexole
pravastatin
prazosin
prednisolone
prednisone
primaquine
primethamine
primidone
probencid
probucol
procainamide
procarbazine
progestins
promethazine
propafenone
propantheline
propoxyphene
propranolol

propulsid
pseudoephedrine
psoralens
psyllium
pyridostigmine
pyridoxine (vitamin b-6)
quinacrine
quinapril
quinidine
quinine
rabeprazole
raloxifene
ramipril
ranitidine
recombinant clotting factor VIII
recombinant interferon alpha-2b
recombinant OspA
remoxipide
reserpine
rezulin
ribavirin
nifampin
rimantadine
risedronate
risperidone
ritodrine
rosiglitazone
salicylates
salmeterol
saquinavir
scopolamine
selcane
selegiline
sertraline
sibutramine
sildenafil citrate
simethicone
simvastatin
s-mephenytoin
sodium ferric gluconate
soman
somatostatin
sotalol
spironolactone
stanol esters
streptozotocin

succinimide
sucralfate
sulfacytine
sulfadoxine
sulfamethoxazole
sulfamethoxazole
sulfasalazine
sulfapyrazone
sulfisoxazole
sumatriptan
(S)-warfarin
tacrine
tamoxifen
tamsulosin
telmisartan
temazepam
terazosin
terbinafine HCl
terbutaline sulfate
terfenadine
terpin hydrate
testolactone
tetracycline HCl
tetracyclines
theophylline
thiamine
thiazide
thioguanine
thiopurine
thiothixene
tiagabine
ticlopidine
tienilic acid
timolol
tiopronin
tirofiban
tobramycin
tobramycin/dexamethasone
tocainide
tolbumamide
tolcapone
tolterodine
topotecan
toremifene
tramadol
trandolapril

trastuzumab
trazodone
tretinoin
triamcinolone
triamterene/HCTZ
triamterine
triamterine
triazolam
trihexyphenidyl
trilostane
trimeth/sulfameth
trimethobenzamide
trimethoprim
troglitazone
trovafloxacin
urokinase
ursodiol
valproic acid
valsartan
vancomycin
venlafaxine
verapamil
vincristine
warfarin
xanthine
xylometazoline
zaflirlukast
zalcitabine
zidovudine
zolpidem

**TABLE 2**

<b>Industrial Chemicals</b>
1,2-Dibromomethane
2,4-dinitrotoluene
2-methylpentane
3-methylpentane
4,4'-methylene bis
7, 12-dimethylbenz[a]anthracene
Acetone
Acrylamide
Acrylonitrile
Apha methylstyrene
Aluminum
Aniline
Antimony
Arsenic
Barium
Baygon
Benzene
Benzidine
Berylium
Bta-naphthylamine
Biphenyl
Cadmium
Carbamate(s)
Carbaryl
Carbon disulfide
Carbon monoxide
Carbon tetrachloride
Chloroform
Chromium VI
Cobalt
Copper
Cumene
Cyanamide
Cyanides
Cyclohexane
Cyclohexanone
Cyclophosphamide
DDT
DEHP
Dichlorobenzene
Dichloromethane

Dieldrin
Diethylamine
Diethylstilbestrol
Dimethylacetamide
Dimethylformamide
Dinitroorthocresol
Dioxane
Endrin
Enflurane
Ethylbenzene
Ethylene oxide
Ethyleneglycol dinitrate
Ethyleneglycol(s)
Fluoride
Furfural
Furfuryl alcohol
Germanium
Halothane
Hexachlorobenzene
Hexachlorobutadiene
Isopropanol
Isopropyl nitrate
Lead
Lead tetraethyl
Lindane
Maleic anhydride
Manganese
Mercury
Methanol
Methylchloride
Methylethylketone
Methylmercury
Monobromomethane
Monochlorobenzene
n-hexane
Nickel
Nitrobenzene
Nitroglycerine
Nitrous oxide
Organophosphorus
Parathione
Pentachlorophenol
Phenol
Phthalic anhydride
Polychlorinated biphenyl
Polycyclic hydrocarbons

Propyleneglycol
Selenium
Silver
Stryrene
Synthetic pyrethroids
T-butylhydroperoxide
TCDD
Tellerium
Tert-butylphenol
Tetrachloroethylene
Thalium
Toluene
Toluene diisocyanate
Trichloroethane
Trichloroethylene
Triethylamine
Triethylbenzenes
Uranium
Vanadium
Vinyl chloride
Xylene
Zinc

TABLE 3

Gene Name	Genbank Accession No.
Ataxia telangiectasia	U33841
ATF4 (activating trxn factor 4)	D90209
ATP-dep. Helicase II (70kDa)	M32865
ATP-dep. Helicase II (Ku80)	M30938
Bax (alpha)	L22473
Bcl-xL	Z23115
c-Abl	M14752
c-Fos	K00650
Chk1	AF016582
c-H-Ras	J00277
c-Jun	J04111
Clusterin (serum protein 40)	X14723
c-Myc	X00364
Connexin 32 (gap junction protein)	X04325
Cyclin G	D78341
Cytochrome P-1-450 (cyp1A1)	K03191
DNA binding protein inhibitor ID-2	D13891
DNA dependent helicase	L36140
DNA dependent protein kinase	U47077
DNA ligase IV	X83441
DNA polymerase alpha	X06745
DNA repair protein (Rad 50)	U63139
DNA repair protein XRCC1	M36089
DNA topoisomerase I	J03250
ERCC1 (excision repair protein)	M13194
DNA repair helicase II ERCC-3	M31899
Excision repair ERCC-5	L20046
Gadd153	S40706
Gadd45	M60974
Glutathione Peroxidase	M21304
HDLC1	U32944
Hsp70	M11717
Hsp90	X15183
ICE Rel II	U28014
Mdm-2	U33199
Mdr-1	M14758
MnSOD	Y00985
Mut S homologue (hMSH2)	U04045
MUTL homolog=hMLH1	U07418
Poly (ADP-ribose) polymerase (PARP)	M32721/X56140
Prolifer.cell nuclear antigen (PCNA)	J04718
RAD	L24564

RAD51 homolog	D13804
RNA-dependent Helicase (DEAD-box protein p72)	U59321
SQM1	M33374
Stress activated protein kinase JNK1	L26318
UV Excision repair protein RAD23 (XP-C)	D21090
Vascular cell adhesion molecule 1 (VCAM-1)	M73255
Alpha-Tubulin	K00558
Beta-Actin	X00351
Glucose-6-phosphate dehydrogenase (G6PD)	X03674
cytochrome p-450 4A	L04751
connexin 40	L34954
Bak	U16811
Collagenase, type I interstitial	X54925
G/T mismatch binding protein	U28946
Mismatch repair/binding protein (hMSH3)	U61981
DNA mismatch repair protein (hPMS2)	U14658
Apolipoprotein A-II	M29882
Acyl CoA dehydrogenase	U12778
Carnitine palmitoyl CoA transferase	M58581
Hepatic lipase	J03540
Ornithine decarboxylase	M16650
Superoxide dismutase Cu/Zn (SOD)	K00065
Ref-1=redox factor	S43127
Thioredoxin	J04026
Glutathione synthetase	L42531
Glutathione reductase	X15722
Thymidine kinase	K02581
Bag-1=bcl-2	S83171
BRCA1	U14680
Phenol sulfotransferase	U26309
Aldehyde dehydrogenase 1 (ALDH-1)	K03000
Aldehyde dehydrogenase 2 (ALDH-2)	K03001
12-lipoxygenase	M58704
Phospholipase A2	M86400
Calnexin	M94859
Apolipoprotein CIII.	X01388
Branched chain Acyl-CoA Oxidase	X95190
Cyclin dependent kinase 4 (cdk4)	M14505
ERp72	J05016
MCL-1	L08246
HMG CoA reductase	M11058
Lipopolysaccharide binding protein	M35533
Lysyl oxidase	M94054
Farnesol Receptor	U68233
Osteopontin	J04765
P38 mitogen activated protein (MAP) kinase	L35253
Peroxisomal acyl-CoA oxidase	X71440

Uncoupling protein 2 (UCP2)	U82819
Very-long-chain acyl-CoA dehydrogenase	D43682
Vimentin	X56134
EGR1	X52541
GRP94	X15187
P53	K03199
Defender against cell death-1	D15057
Hypoxanthine-guanine phosphoribosyltransferase	V00530
Aspartate aminotransferase, mitochondrial	M22632
Creatine kinase B	L47647
Peroxisome assembly factor-1	M86852
T-cell cyclophilin	Y00052
Transferrin	M12530
UDP-glucuronosyltransferase 2B	AF016492
Octamer-binding protein 1	X13403
E-cadherin	L08599
Catalase	X04076
11 beta-hydroxysteroid dehydrogenase type II	U14631
Bilirubin UDP-glucuronosyltransferase isozyme 1	M57899
Calreticulin	M84739
Calcineurin-B	M30773
Catechol-O-methyltransferase	M58525
Fas antigen	M67454
DNA repair and recombination homologue (RAD52)	L33262
Flavin-containing monooxygenase 1	M64082
Gamma-glutamyl transpeptidase	L20490
Insulin-like growth factor binding protein 1	M31145
Oxygen-regulated protein 150	U65785
Thymidylate synthase	X02308
Biliverdin reductase	U34877
Adenine nucleotide translocator 1	J02966
Hepatocyte nuclear factor 4	X76930
RANTES	M21121
Phosphoglycerate kinase	V00572
PAPS synthetase	Y10387
Plasminogen activator inhibitor 2	M18082
Enolase alpha	M14328
Interferon inducible protein 15	M13755
Insulin-like growth factor I	M37484
Platelet/endothelial cell adhesion molecule-1	M28526
60S ribosomal protein L6	X69391
FosB	L49169
Alpha-catenin	D13866
FEN-1 (endonuclease)	L37374
GOS24 (zinc finger transcriptional regulator)	M92843
Caspase 8 (FLICE)	U58143
Caspase 3 (CPP32-beta)	U13738

Caspase 7 (Mch3-alpha)	U37448
Intercellular adhesion molecule-3	X69819
Phosphoenolpyruvate carboxykinase	X92720
Alpha-1 acid glycoprotein	M13692
IkB-a	M69043
Protein-tyrosine phosphatase	M83738
Ubiquitin conjugating enzyme (Rad6 homolog)	M74524
Alpha-2-macroglobulin	M11313
Zinc finger protein 37	AF022158
Cyclin-dependent kinase inhibitor p27kip1	U10906
Caspase 1	U13697
Organic anion transporter 1	AF057039
Alcohol dehydrogenase 2	M24317
Alcohol dehydrogenase 4	M15943
Annexin V	M21731
Calbindin-D (28kDa)	X06661
Colony-stimulating factor-1	M37435
Hypoxia-inducible factor 1 alpha	U22431
Growth arrest-specific protein 1	L13698
Inhibitor of apoptosis protein-1	AF070674
Nucleic acid binding protein	U19765
OX40 ligand	X79929
Retinoic acid receptor gamma 1	M38258
Cytochrome c oxidase subunit IV	M34600
Glutathione S-transferase theta-1	X79389
Survivin	NM001168
STAT 3	AJ012463
Growth arrest-specific protein 3	L03203
Cyclin D3	M92287
ID-1	X77956
Interleukin-1 beta	X02532
Interleukin-8	Y00787
Monocyte chemotactic protein-1	S69738
Phenylalanine hydroxylase	K03020
Prohibitin	S85655
Cathepsin L	M20496
Transthyretin	X59498
Stromelysin-1	X05232
Spermidine/spermine N1-acetyltransferase (SSAT)	M55580
Ferritin H-chain	L20941
Transferrin receptor	M11507
Ceruloplasmin	M13699
Glucosylceramide synthase	D50840
Leukemia inhibitory factor (LIF)	X13967
Integrin beta-1	X07979
Vascular endothelial growth factor receptor 1 (flt-1)	X51602
Urokinase plasminogen activator receptor (uPAR)	U08839

c-fms	X03663
c-erb B-2	X03363
C5a anaphylatoxin receptor	M62505
FYN proto-oncogene	NM002037
Peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase	L07077
Nucleoside diphosphate kinase beta isoform	X73066
Myelin basic protein	M13577
Peroxisomal 3-oxoacyl-CoA thiolase (=rat peroxisomal 3-ketoacyl-CoA thiolase 2)	X12966
Prostaglandin H synthase	S36271
Retinoid X receptor alpha	NM002957
Interleukin-13	X69079
Tryptophanyl-tRNA synthetase (WRS)	M61715
Silencer of death domains	AF111116
Mannose receptor	J05550
Death receptor 5 (DR5)	AF016268

Neomycin

U55761

**TABLE 4**

(clone hKvBeta3) K<sup>+</sup> channel beta subunit  
 APO-1 cell surface antigen  
 11-beta hydroxysteroid dehydrogenase type II  
 12-lipoxygenase  
 17-beta hydroxysteroid dehydrogenase  
 25-hydroxyvitamin D3-1 alpha-hydroxylase  
 60S ribosomal protein L6  
 6-C-kine  
 6-O-methylguanine-DNA methyltransferase  
 acetylhydrolase IB beta-subunit  
 Acid ceramidase  
 actin-binding protein (filamin) (ABP-280)  
 Activating transcription factor 2  
 Activating transcription factor 3  
 Activating transcription factor 4  
 Activin beta E  
 Activin receptor type II  
 Acyl - CoA dehydrogenase  
 Acyl CoA Carrier Protein  
 Adenine nucleotide translocator 1  
 Adenylyl cyclase-associated protein (CAP)  
 Adhesion protein (SQM1)  
 Alanine aminotransferase  
 Alcohol dehydrogenase 1  
 Alcohol dehydrogenase 2  
 Alcohol dehydrogenase 3  
 Alcohol dehydrogenase 4  
 Alcohol dehydrogenase 7  
 Aldehyde dehydrogenase 1  
 Aldehyde dehydrogenase 2  
 Aldehyde dehydrogenase 3  
 Aldose reductase  
 Alpha 1-antitrypsin  
 Alpha 1-inhibitor III  
 Alpha interferon  
 Alpha(I)procollagen  
 Alpha-1 acid glycoprotein  
 Alpha-1 antichymotrypsin  
 Alpha-2 macroglobulin  
 Alpha-2 microglobulin  
 Alpha-catenin  
 Alpha-tubulin  
 Amyloid protein homologue  
 Androgen receptor  
 Annexin V

Antiquitin, 26g turgor protein homolog  
Aorta caldesmon  
APC gene  
Apolipoprotein A1  
Apolipoprotein AII  
Apolipoprotein CIII  
Apolipoprotein E  
Aryl hydrocarbon receptor  
Aspartate aminotransferase, mitochondrial  
Ataxia telangiectasia  
ATP Synthase 6  
ATP-dependent helicase II (70kDa)  
ATP-dependent helicase II (Ku80)  
Atrial natriuretic factor  
BAG-1  
BAK  
Bax (alpha)  
Bcl-2  
Bcl-3  
Bcl-xL  
Beta-actin  
Beta-chemokine I-309  
Bile salt export pump (sister of p-glycoprotein)  
Biliary glycoprotein  
Bilirubin UDP-glucuronosyltransferase isozyme 1  
Biliverdin reductase  
B-myb  
Bone morphogenetic protein-4  
Bone sialoprotein gene  
Brain-derived neurotrophic factor  
Branched chain acyl-CoA oxidase  
BRCA1  
BR-cadherin  
Breast basic conserved gene (ribosomal protein L13)  
Breast cancer resistance protein (BCRP)  
C10 beta-chemokine  
C4b-binding protein  
C5a anaphylatoxin receptor  
c-abl  
Calbindin-D (28kDa)  
Calbindin-D (9K)  
Calcineurin-B  
Calnexin  
Calprotectin  
Calreticulin  
canalicular multispecific organic anion transporter

**Carbonic Anhydrase III**  
**Carcinoembryonic antigen (CD66e)**  
**Carcinoembryonic antigen family member 2**  
**cardiac gap junction protein**  
**Carnitine palmitoyl-CoA transferase**  
**Casein kinase 1 delta**  
**Caspase 1**  
**Caspase 2 (Nedd2)**  
**Caspase 3 (CPP32-beta)**  
**Caspase 5 (ICE rel-III)**  
**Caspase 6 (Mch2-alpha)**  
**Caspase 7 (Mch3-alpha)**  
**Caspase 8 (FLICE)**  
**Catalase**  
**Catechol-O-methyltransferase**  
**Cathepsin G**  
**Cathepsin L**  
**Caveolin-1**  
**CCAAT/enhancer-binding protein alpha**  
**CCAAT/enhancer-binding protein epsilon**  
**CCR-5**  
**CD44 (metastasis suppressor gene)**  
**CD64 (Fc gamma)**  
**Cell division cycle protein 2**  
**Cell division cycle protein 25**  
**Cellular retinoic acid binding protein 1**  
**Cellular retinoic acid binding protein 2**  
**c-erb B-2**  
**c-erbA-1**  
**Ceruloplasmin (ferroxidase)**  
**c-fms (CSF-1 receptor)**  
**c-fos**  
**CHD2**  
**Checkpoint kinase-1**  
**Cholesterol esterase**  
**c-H-ras**  
**CIG49 (cig49)**  
**c-jun**  
**Clone 22 mRNA, alternative splice variant alpha-1**  
**CLP**  
**Clusterin**  
**c-myb**  
**c-myc binding protein**  
**Collagen type II**  
**Colony-stimulating factor-1**  
**Complement component C3**

Connexin 30  
Connexin-32 (aka gap junction protein)  
Connexin-40  
Corticosteroid binding globulin  
Corticotropin releasing hormone  
C-reactive protein  
Creatine kinase B  
Csa-19  
CTCF  
CXCR4  
Cyclin A1  
Cyclin D1  
Cyclin D3  
Cyclin dependent kinase 1  
Cyclin dependent kinase 2  
Cyclin dependent kinase 4  
Cyclin dependent kinase inhibitor 1A  
Cyclin E  
Cyclin G  
Cyclin-dependent kinase 4 inhibitor B (P16)  
Cyclin-dependent kinase inhibitor P27Kip1  
Cyclooxygenase 2  
Cysteine protease CPP32 isoform alpha  
Cystic fibrosis transmembrane conductance regulator  
Cytochrome c oxidase subunit III  
Cytochrome c oxidase subunit IV  
Cytochrome P450 11A1  
Cytochrome P450 17A  
Cytochrome P450 1A1  
Cytochrome P450 1A2  
Cytochrome P450 1B1  
Cytochrome P450 2A1  
Cytochrome P450 2A3  
Cytochrome P450 2A6  
Cytochrome P450 2B1  
Cytochrome P450 2B10  
Cytochrome P450 2B2  
Cytochrome P450 2C11  
Cytochrome P450 2C12  
Cytochrome P450 2C19  
Cytochrome P450 2C9  
Cytochrome P450 2D6  
Cytochrome P450 2E1  
Cytochrome P450 2F2  
Cytochrome P450 3A1  
Cytochrome P450 3A4

Cytochrome P450 4A  
Cytochrome P450 4A1  
cytoskeletal gamma-actin  
Damage-specific DNA binding protein p48  
subunit  
Death receptor 5 (DR5)  
Defender against cell death-1  
Deleted in colorectal cancer  
Delta-like protein  
Diacylglycerol kinase zeta  
Dihydrofolate reductase  
Disulfide isomerase related protein (ERp72)  
DNA binding protein inhibitor ID2  
DNA dependent helicase  
DNA dependent protein kinase  
DNA ligase I  
DNA ligase III  
DNA ligase IV  
DNA mismatch repair protein (MLH1)  
DNA mismatch repair protein (PMS2)  
DNA mismatch repair/binding protein (MSH3)  
DNA polymerase alpha  
DNA polymerase beta  
DNA repair and recombination homologue (RAD  
52)  
DNA repair helicase II ERCC-3  
DNA repair protein (RAD 50)  
DNA repair protein (XRCC1)  
DNA replication factor C (36kDa)  
DNA topoisomerase I  
DNA topoisomerase II  
DNA-binding protein (APRF)  
DOC-2  
Dopamine beta-hydroxylase  
Dopamine receptor D2  
DRA  
Dynamin (DNM)  
Dynein light chain 1  
E2F-1  
Early growth regulated protein 1  
E-Cadherin  
ECE-1 (endothelin converting enzyme)  
ELAV-like neuronal protein-2 Hel-N2  
Elongation factor 1-alpha 1 (PTI-1)  
Endothelin-1  
Enolase alpha  
enteric smooth muscle gamma-actin

Eosinophil-derived neurotoxin  
Eotaxin  
Epidermal growth factor  
Epoxide hydrolase  
ERA-B  
ERCC 1 (excision repair protein)  
ERCC 3 (DNA repair helicase II)  
ERCC 5 (excision repair protein)  
ERCC 6 (excision repair protein)  
Erythrocyte membrane protein  
Erythropoietin  
Erythropoietin receptor  
E-Selectin  
Estrogen receptor  
Extracellular-signal-regulated kinase 1  
Farnesol receptor  
Fas antigen  
Fas associated death domain (FADD)  
Fas ligand  
Fas/Apo1 receptor  
Fatty acid synthase  
Fatty acyl-CoA oxidase  
Fatty acyl-CoA synthase  
FEN-1 (endonuclease)  
Ferritin H-chain  
FGF-1  
FGF-7  
Fibrinogen gamma chain  
Fibronectin receptor  
FIC1  
Filaggrin  
Flavin containing monooxygenase 1  
Flavin containing monooxygenase 3  
for gamma-interferon inducible early response  
gene (with homology to platelet proteins)  
FosB  
Fra-1  
Fucosyl transferase (alpha-1,2-  
fucosyltransferase)  
Fyn proto-oncogene  
Gadd153  
Gadd45  
Galanin  
Gamma glutamylcysteinyl synthetase  
Gamma-glutamyl hydrolase (hGH)  
Gamma-glutamyl hydrolase precursor  
Gamma-glutamyl transpeptidase

Garg-16  
GAS-7  
GCLR  
GCLS  
Gelsolin  
Glucocorticoid receptor  
Glucose-6-phosphate dehydrogenase  
Glucose-regulated protein 170  
Glucose-regulated protein 58  
Glucose-regulated protein 78  
Glucose-regulated protein 94  
Glucosylceramide synthase  
Glutamic-oxaloacetic transaminase  
Glutamic-pyruvic transaminase  
Glutamine synthetase  
Glutaredoxin  
Glutathione peroxidase  
Glutathione reductase  
Glutathione S-transferase alpha subunit  
Glutathione S-transferase theta-1  
Glutathione S-transferase Ya  
Glutathione synthetase  
Glyceraldehyde 3-phosphate dehydrogenase  
Gonadotropin (alpha subunit)  
GOS24 (zinc finger transcriptional regulator)  
Granulin  
Granulocyte-macrophage colony-stimulating factor  
Growth arrest-specific protein 1  
Growth arrest-specific protein 3  
GT mismatch binding protein  
Hamartin (TSC1)  
H-cadherin  
Heat shock protein 12  
Heat shock protein 27  
Heat shock protein 47  
Heat shock protein 70  
Heat shock protein 90  
Helicase-like transcription factor  
Heme binding protein 23  
Heme oxygenase-1  
Hemopexin  
Hepatic lipase  
Hepatocyte growth factor  
Hepatocyte growth factor activator  
Hepatocyte nuclear factor 4  
Histamine N-methyltransferase

Histidine decarboxylase  
Histone 2A  
Histone 2B  
Histone deacetylase 1 (HDAC-1)  
hMEF2C, myocyte enhancer-binding factor 2  
HMG CoA reductase  
HMG-I protein isoform mRNA (HMGI gene),  
clone 7C  
Hydroxysteroid sulfotransferase a  
Hypoxanthine-guanine  
phosphoribosyltransferase  
Hypoxia-inducible factor 1 alpha  
ICE-rel II (Caspase 4)  
ID-1  
IkB-a  
immunoglobulin lambda heavy chain  
Immunophilin homolog ARA9  
Inhibitor of apoptosis protein 1  
Inhibitor of apoptosis protein 2  
Insulin-like growth factor binding protein 1  
Insulin-like growth factor binding protein 2  
Insulin-like growth factor binding protein 5  
Insulin-like growth factor binding protein 3  
Insulin-like growth factor I  
Insulin-like growth factor II  
Integrin alpha  
Integrin alpha L  
Integrin beta1  
Integrin beta2  
Integrin beta-4  
Intercellular adhesion molecule-1  
Intercellular adhesion molecule-2  
Intercellular adhesion molecule-3  
Interferon gamma  
Interferon inducible protein 10  
Interferon inducible protein 15  
Interferon stimulatory gene factor-3  
Interleukin-1 alpha  
Interleukin-1 beta  
Interleukin-10  
Interleukin-12  
Interleukin-13  
Interleukin-18  
Interleukin-2  
Interleukin-3  
Interleukin-4  
Interleukin-5

Interleukin-6  
Interleukin-8  
Involucrin  
IRF-7  
Iron permease (FTR1)  
ISG-15  
Jagged 1  
Jagged 2  
JNK1 stress activated protein kinase  
JunB  
JunD  
K<sup>+</sup> channel beta 2 subunit  
KAI1 metastasis suppressor gene (CD82)  
K-cadherin  
Keratin 4  
Keratin 6 isoform K6e (KRT6E)  
Keratin K17  
Keratinocyte growth factor  
Ki67  
Ku autoimmune antigen gene (p80)  
L09604  
Lactate Dehydrogenase-B  
Lactoferrin  
Leukemia inhibitory factor (LIF)  
Lipopopolysaccharide binding protein  
Lipoprotein lipase precursor  
Liposin  
Liver fatty acid binding protein  
L-myc  
long-chain acyl-CoA synthetase  
Low density lipoprotein receptor  
Lung cancer antigen NY-LU-12 variant A  
Luteinizing hormone  
Lymphoid enhancer-binding factor-1 (LEF-1)  
Lysyl hydroxylase  
Lysyl oxidase  
macropain subunit zeta  
Macrophage inflammatory protein-1 alpha  
Macrophage inflammatory protein-1 beta  
Macrophage inflammatory protein-2 alpha  
Macrophage inflammatory protein-3 alpha  
Macrophage-stimulating protein (MST1)  
Macrostatin  
MAD-related protein 2  
Major acute phase protein alpha-1  
Major basic protein  
Malic enzyme

Mannose receptor  
MAP kinase kinase  
Matrix metalloproteinase-1  
Matrix metalloproteinase-2  
MDM-2  
MET proto-oncogene  
Metallothionein 1  
Metallothionein 2  
Metal-regulatory transcription factor-1  
Metastasis-associated mta1  
Methionine adenosyltransferase (MAT2A)  
MHC class I  
MHC class II  
MHC class II transactivator  
Mim  
Mitochondrial ATP Synthase Subunit E  
mitochondrial short-chain enoyl-CoA hydratase  
Mitochondrial transcription factor 1  
Mitogen activated protein kinase (P38)  
Mitogen inducible gene (mig-2)  
MOAT-B (MRP/organic anion transporter)  
Monoamine oxidase A  
Monoamine oxidase B  
Monocyte chemotactic protein-1  
Monocyte chemotactic protein-1 receptor (CCR2)  
Mr 110,000 antigen  
MSH3 gene  
mss4, Zn<sup>2+</sup> binding protein/guanine nucleotide exchange factor  
Multidrug resistance-associated protein  
Multidrug resistant protein-1  
Multidrug resistant protein-2  
Multidrug resistant protein-3 = cMOAT2  
MUTL homologue (MLH1)  
MutS Homologue (MSH2)  
Myelin basic protein  
Myeloid cell differentiation protein-1  
Myeloid cell leukemia-1 (MCL-1)  
Myeloperoxidase  
Na/taurocholate cotransporting polypeptide  
NADPH cytochrome P450 reductase  
NADPH quinone oxidoreductase-1 (DT-Diaphorase)  
Natural killer cell-enhancing factor B  
N-cadherin  
Neural cell adhesion molecule (N-CAM)  
Neurofibromin (NF1 tumor suppressor)

neuropathy target esterase  
NF-E2  
NF-kappaB (p65)  
Nidogen  
Nitric oxide synthase-1, inducible  
NMB  
Non-specific cross-reacting antigen  
Notch 1  
Nucleic acid binding protein  
Nucleoside diphosphate kinase beta isoform  
nucleosome assembly protein  
O-6-alkylguanine-DNA-alkyltransferase  
OB-cadherin 1  
Octamer binding protein 1  
Octamer binding protein 2  
Oncostatin M  
Organic anion transporter 1  
Organic anion transporter 3  
Organic anion transporter K1  
Organic anion transporting polypeptide 1  
Organic cation transporter 1  
Organic cation transporter 2  
Organic cation transporter N1  
Organic cation transporter N2  
Ornithine decarboxylase  
Osteocalcin  
Osteopontin  
Osteoprotegerin (TRAIL/Apo2L receptor)  
OTK27  
OX40 ligand  
Oxygen regulated protein 150  
Oxysterol-binding protein (OSBP)  
Oxytocin receptor  
p190-B (p190-B)  
P311 HUM (3.1)  
p53  
p55CDC  
p70 ribosomal protein S6 kinase alpha-1  
Pancreatitis-associated protein  
PAPS synthetase  
PBX2 mRNA  
P-cadherin  
PCDH7 (BH-Pcdh)c  
PDGF associated protein  
PEG3  
Perlecan  
Peroxisomal 3-ketoacyl-CoA thiolase 1

Peroxisomal 3-ketoacyl-CoA thiolase 2  
Peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase  
Peroxisomal fatty acyl-CoA oxidase  
Peroxisome assembly factor 1  
Peroxisome assembly factor 2  
Peroxisome biogenesis disorder protein-1  
Peroxisome biogenesis disorder protein-11  
Peroxisome biogenesis disorder protein-4  
Peroxisome hydratase  
Peroxisome proliferator activated receptor alpha  
Peroxisome proliferator activated receptor gamma  
Phenol sulfotransferase  
Phenylalanine hydroxylase  
Phosphatase 2A B56-alpha (PP2A)  
Phosphoenolpyruvate carboxykinase  
Phosphoglyceride kinase  
Phospholipase A2  
Phosphomannomutase (PMM2)  
Pim1 proto-oncogene  
Plasma cell membrane glycoprotein  
plasma gelsolin  
Plasminogen activator inhibitor 2  
Platelet derived growth factor B  
Platelet/endothelial cell adhesion molecule-1  
Poly(ADP-ribose) polymerase  
polyA binding protein  
Presenilin-1  
Prion protein (PrP)  
pro-cathepsin L (major excreted protein MEP)  
Progesterone receptor  
Prohibitin  
Prolidase  
Proliferating cell nuclear antigen gene  
Proliferation-associated gene A (natural killer-enhancing factor A)  
prolyl 4-hydroxylase beta subunit (EC 1.14.11.2)  
(procollagen-L-proline, 2-oxoglutarate:oxygen oxidoreductase, 4-hydroxylating)  
Prostacyclin-stimulating factor (IGFBP-7)  
Prostaglandin H synthase  
Prostate-specific antigen  
protein disulfide isomerase  
Protein kinase C alpha  
Protein tyrosine phosphatase alpha  
Protein-tyrosine phosphatase

Psoriasin 1 (S100 calcium-binding protein A7)  
PTEN/MMAC1  
Putative cyclin G1 interacting protein  
Quinone reductase (zeta-crystallin)  
RAD  
RAD 51 homologue  
RANTES  
RAP1A (ras-related protein)  
Recombination activating gene 1 (RAG-1)  
Ref-1  
RelB  
Replication factor C, 40-kDa subunit (A1)  
Replication protein A (70 kDa subunit)  
Retinoblastoma  
Retinoblastoma related protein (P107)  
Retinoic acid receptor beta  
Retinoic acid receptor gamma-1  
Retinoid X receptor alpha  
Retinoid X receptor beta  
Retinoid X receptor gamma  
Ribonucleotide reductase M1 subunit  
Ribosomal protein L13A  
Ribosomal protein L34 (RPL34)  
Ribosomal protein L37a (RPL37A)  
ribosomal protein S12  
Ribosomal protein S4 (RPS4X) isoform  
Ribosomal protein S9  
RNA-dependent helicase  
SAA-3  
S-adenosylmethionine synthetase  
Sarcoplasmic reticulum calcium ATPase  
Sarcosin  
Sec23B isoform, 2450bp  
Senescence marker protein-30  
Serine kinase  
Serum amyloid A1  
Serum amyloid A2-alpha  
Serum response factor  
Silencer of death domains (SODD)  
Small proline-rich protein (spri)  
SMT3A protein  
SMT3B protein  
snRNP polypeptide B  
Sodium/bile acid cotransporter  
Sonic hedgehog gene  
Sorbitol Dehydrogenase  
SoxS

SPARC (secreted protein acidic and rich in cysteine)  
Spermidine/spermine N1-acetyltransferase (SSAT)  
Sphingomyelinase (neutral)  
STAT 1  
STAT 2  
STAT 3  
Stem cell factor  
Steroid hormone receptor Ner-I  
Sterol carrier protein 2  
Sterol regulatory element binding protein-2  
Stromelysin-1  
Superoxide Dismutase Cu/Zn  
Superoxide dismutase Mn  
Suppressor of cytokine signaling 1 (SOCS-1)  
Suppressor of cytokine signaling 3 (SOCS-3)  
Survivin  
Synapsin I  
Synaptophysin II  
Synaptotagmin I  
Syntaxin 3  
Tau protein  
T-cell activation gene 3  
T-cell cyclophilin  
T-cell mRNA for glycyl tRNA synthetase  
T-cell receptor  
Tenascin  
Thiol-specific antioxidant protein mRNA  
Thiopurine methyltransferase  
Thioredoxin  
Thrombin receptor (PAR-1)  
Thrombomodulin  
Thrombospondin 2  
Thymidine kinase  
Thymidylate synthase  
Thymosin beta-10  
Tight junction protein Zo-1  
Tissue factor  
Tissue factor pathway inhibitor  
Tissue inhibitor of metalloproteinases-1  
Tissue inhibitor of metalloproteinases-3  
Tissue transglutaminase  
TNF receptor-1 associated protein (TRADD)  
transcription elongation factor S-II, hS-II-T1  
Transcription factor IID  
transcriptional activator hSNF2b

Transferrin  
Transferrin receptor  
Transforming growth factor-beta 3  
Transthyretin  
Tropoelastin  
Tryptophan hydroxylase  
Tryptophanyl-tRNA synthetase  
ts11 gene encoding a G-1 progression protein  
Tumor necrosis factor associated factor 2  
(TRAF2)  
Tumor necrosis factor receptor 1  
Tumor necrosis factor receptor 2  
Tumor necrosis factor receptor-1 associated  
protein (TRADD)  
Tumor necrosis factor-alpha  
Tumor necrosis factor-beta  
Type 1 interstitial collagenase  
Tyrosine aminotransferase  
Tyrosine hydroxylase  
Tyrosine protein kinase receptor (UFO)  
U1 small nuclear RNP-specific C protein  
Ubiquitin  
Ubiquitin conjugating enzyme (Rad 6 homologue)  
Ubiquitin conjugating enzyme G2 (UBE2G2)  
Ubiquitin-homology domain protein PIC1  
UDP-glucuronosyltransferase 2  
UDP-glucuronosyltransferase 2B  
Uncoupling protein 1  
Uncoupling protein 2  
Uncoupling protein 3  
Urate oxidase  
Urokinase plasminogen activator receptor  
(uPAR)  
UV excision repair protein RAD 23 (XP-C)  
Vascular cell adhesion molecule 1 (VCAM-1)  
Vascular endothelial growth factor  
Vascular endothelial growth factor D  
Vascular endothelial growth factor receptor 1 (flt-  
1)  
Very long-chain acyl-CoA dehydrogenase  
Vesicle-associated membrane protein-2 (VAMP-  
2)  
Vesicular acetylcholine transporter (VACHT)  
Vesicular monoamine transporter (VMAT)  
Vimentin  
Visinin-like peptide 1 homolog  
Vitellogenin

**Waf1**  
**Wnt-13 mRNA**  
**X13694**  
**Zinc finger protein ZNF134**  
**Zinc finger protein**  
**Zinc-finger DNA-binding motifs (IA-1)**  
**Zinc-finger protein-37**  
**Zipper protein kinase (ZPK)**  
**Serum paraoxonase**

5

TABLE 5

<b>Renal Toxicity</b>	<b>Neural Toxicity</b>
Alpha-2 microglobulin	Acid ceramidase
Bile salt export pump (sister of p-glycoprotein)	Ataxia telangiectasia
Calbindin-D (28kDa)	Brain-derived neurotrophic factor
Calbindin-D (9K)	Brain-derived neurotrophic factor
Calcineurin-B	Choline kinase
Calnexin	Cystic fibrosis transmembrane conductance regulator
Cholesterol esterase	Dopamine beta-hydroxylase
endothelin-1	Dopamine receptor D2
FGF-1	Dopamine transporter
FGF-7	Endothelin-1
Gamma glutamylcysteinyl synthetase	Glial fibrillary acidic protein
Gamma-glutamyl hydrolase precursor	Glutamine synthetase
Gamma-glutamyl transpeptidase	Myelin basic protein
Heat shock protein 90	Nerve growth factor
Kidney injury molecule-1	Nerve growth factor receptor
NMB	Neural cell adhesion molecule
Organic anion transporter 1	Neuropathy target esterase
Organic cation transporter 1	Synapsin I
p-glycoprotein (MDR-1)	Synaptophysin
Phosphoenolpyruvate carboxykinase	Synaptotagmin I
Sphingomyelinase, neutral	Tau protein
Vimentin	Vesicular acetylcholine transporter
MOAT-B (MRP/organic anion transporter)	Vesicular monoamine transporter
Organic anion transporter 1	Norepinephrine transporter
Organic anion transporter 3	Serotonin N-acetyltransferase
Organic anion transporter K1	Serotonin transporter (SERT)
Organic anion transporting polypeptide 1	Sphingomyelinase (neutral)
Organic cation transporter 1	
Organic cation transporter 2	
Organic cation transporter 3	
Osteopontin	
Renal organic anion transporter	

Hepatic Toxicity	Immunotoxicity
11-beta hydroxysteroid dehydrogenase type II	6-C-kine
12-lipoxygenase	Complement component C3
15-hydroxyprostaglandin dehydrogenase	Cyclooxygenase 2
17-beta hydroxysteroid dehydrogenase	Eosinophil-derived neurotoxin
25-hydroxyvitamin D3-1 alpha-hydroxylase	Eotaxin
Alanine aminotransferase	Granulocyte-macrophage colony-stimulating factor
Alcohol dehydrogenase 1	IkB-a
All Cytochrome P450 genes	Interferon gamma
Alpha 1-antitrypsin	Interferon inducible protein 10
Bile salt export pump (sister of p-glycoprotein)	Interferon inducible protein 15
Bilirubin UDP-glucuronosyltransferase isozyme 1	Interferon stimulatory gene factor-3
Biliverdin reductase	Interleukin-1 alpha
Branched chain acyl-CoA oxidase	Interleukin-1 beta
Canalicular multispecific organic anion transporter	Interleukin-10
Carnitine palmitoyl-CoA transferase	Interleukin-12
Catechol-O-methyltransferase	Interleukin-13
Cholesterol esterase	Interleukin-18
Corticosteroid binding globulin	Interleukin-2
Enoyl CoA hydratase	Interleukin-8
Epoxide hydrolase	Interleukin-4
Fatty acid synthase	Interleukin-5
Fatty acyl-CoA oxidase	Interleukin-6
Fatty acyl-CoA synthase	Macrophage inflammatory protein-1 alpha
Flavin containing monooxygenase 1	Macrophage inflammatory protein-1 beta
Focal adhesion kinase (pp125FAK)	Macrophage inflammatory protein-2 alpha
Gamma glutamylcysteinyl synthetase	Macrophage inflammatory protein-2 beta
Gamma-glutamyl hydrolase precursor	Macrophage inflammatory protein-3 alpha
Gamma-glutamyl transpeptidase	Macrophage inflammatory protein-3 beta
Glucose-regulated protein 58	Macrophage metalloelastase
Glutamic-oxaloacetic transaminase	MHC class 1
Glutamic-pyruvic transaminase	MHC class 2
Glutathione S-transferase Ya	MHC class 2 transactivator
Hepatic lipase	Monocyte chemotactic protein receptor (CCR2)
Hepatocyte growth factor	Monocyte chemotactic protein-1
Hepatocyte growth factor receptor	Neutrophil elastase
Hydroxysteroid sulfotransferase a	Phospholipase A2
Na/taurocholate cotransporting polypeptide	

Senescence-marker protein-30	Suppressor of cytokine signaling 1
Hepatocyte growth factor activator	Suppressor of cytokine signaling 3
Lipopolysaccharide binding protein	T-cell activation gene 3
Liver fatty acid binding protein	T-cell cyclophilin
Major acute phase protein alpha-1	
NADPH cytochrome P450 reductase	
Peroxisomal 3-ketoacyl-CoA thiolase 1	
Peroxisomal 3-ketoacyl-CoA thiolase 2	
Peroxisomal acyl-CoA oxidase	
Peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase	
Peroxisomal fatty acyl-CoA oxidase	
Peroxisome assembly factor 1	
Peroxisome assembly factor 2	
Peroxisome biogenesis disorder protein-1	
Peroxisome biogenesis disorder protein-11	
Peroxisome biogenesis disorder protein-4	
Peroxisome hydratase	
Peroxisome proliferator activated receptor alpha	
Peroxisome proliferator activated receptor gamma	
Serum amyloid A1	
Serum amyloid A2-alpha	
Transthyretin	

Cardiotoxicity	Pulmonary Toxicity
Adrenomedullin	GARG-16
Atrial natriuretic factor	GAS-7
Endothelin-1	IRF-7
Glucose transporter 1	ISG-15
Nitric oxide synthase-1, inducible	Lipocalin
Osteopontin	Liposin
Protein kinase C - beta 1	Macrostatin
RhoA	MME
Sarcoplasmic reticulum calcium ATPase	MRP14
Vascular endothelial growth factor	MRP-8 Osteopontin SAA-1 SAA-3 Tenascin Tropoelastin

**TABLE 6**

<b>Apoptosis</b>	<b>Cell Cycle</b>
Adenine nucleotide translocator 1	Activating transcription factor 2
Annexin V	Ataxia telangiectasia
BAK	c-myc
Bax (alpha)	Cell division cycle protein 2
Bcl-xL	Cell division cycle protein 20
c-myc	Cell division cycle protein 25
Calcineurin-B	Checkpoint kinase-1
Calprotectin	Cyclin D1
Caspase 1	Cyclin dependent kinase 1
Caspase 2	Cyclin dependent kinase 4
Caspase 3	Cyclin dependent kinase inhibitor 1A
Caspase 4	Cyclin E
Caspase 6	Cyclin G
Caspase 7	Cyclin-dependent kinase 4 inhibitor B (P15)
Caspase 8	Cyclin-dependent kinase 4 inhibitor B (P16)
Clusterin	Cyclin-dependent kinase 4 inhibitor P27kip1
Cyclin dependent kinase inhibitor 1A	Dihydrofolate reductase
Cyclin-dependent kinase 4 inhibitor	DNA binding protein inhibitor ID2
P27kip1	
Dynein light chain 1	E2F-1
E2F-1	GOS24 (zinc finger transcriptional regulator)
Fas antigen	MDM-2
Fas associated death domain (FADD)	p53
Fas ligand	p55CDC
Gadd153	Retinoblastoma
Interleukin-12	T-cell cyclophilin
p53	Transcription factor IID
Retinoblastoma	Ubiquitin-homology domain protein PIC1
Thymosin beta-10	Waf1
Tumor necrosis factor receptor 1	
Tumor necrosis factor receptor-1 associated protein (TRADD)	
Waf1	

Cell Proliferation	DNA Damage
Activin beta E	Activating transcription factor 2
Activin receptor type II	Ataxia telangiectasia
c-abl	ATP-dependent helicase II (70kDa)
c-erb A-1	ATP-dependent helicase II (Ku80)
c-fos	BRCA1
c-jun	c-abl
c-myc	Cell division cycle protein 20
Early growth regulated protein 1	Checkpoint kinase-1
Endothelin-1	Cyclin D1
Extracellular-signal-regulated kinase 1	Cyclin-dependent kinase 4 inhibitor B (P16)
FosB	DNA dependent protein kinase
GOS24 (zinc finger transcriptional regulator)	DNA ligase I
GT mismatch binding protein	DNA ligase IV
Hepatocyte growth factor receptor ID-1	DNA polymerase beta
Insulin-like growth factor II	DNA repair and recombination homologue (RAD 52)
Interleukin-6	DNA repair protein (RAD 50)
L-myc	DNA topoisomerase I
MutS homologue (MSH2)	DNA topoisomerase II
Proliferating cell nuclear antigen gene	Dynein light chain 1
Replication protein A (70 kDa subunit)	ERCC 1 (excision repair protein)
Ribosomal protein L13A	ERCC 3 (DNA repair helicase II)
Thrombospondin 2	ERCC 5 (excision repair protein)
Thymidine kinase	ERCC 6 (excision repair protein)
Thymidylate synthase	FEN-1 (endonuclease)
Transforming growth factor-beta3	Gadd153
	Gadd45
	GT mismatch binding protein
	JNK1 stress activated protein kinase
	L-myc
	MDM-2
	MutS homologue (MSH2)
	Nucleoside diphosphate kinase beta isoform
	O-6-alkylguanine-DNA-alkyltransferase
	p53
	p55CDC
	Poly(ADP-ribose) polymerase
	Proliferating cell nuclear antigen gene
	RAD 51 homologue
	Ref-1

Replication protein A (70 kDa subunit)  
Retinoblastoma  
Transcription factor IID  
Ubiquitin conjugating enzyme (RAD 6 homologue)  
UV excision repair protein RAD 23 (XP-C)  
Waf1

Inflammation	Peroxisome Proliferation
12-lipoxygenase	17-beta hydroxysteroid dehydrogenase
Apolipoprotein AI	Apolipoprotein CIII
C-reactive protein	Bilirubin UDP-glucuronosyltransferase isozyme 1
Calprotectin	Branched chain acyl-CoA oxidase
Cyclooxygenase 2	Camitine palmitoyl-CoA transferase
Fas ligand	Cytochrome P450 4A
IkB-a	Cytochrome P450 4A1
Intercellular adhesion molecule-1	Enoyl CoA hydratase
Interleukin-1 alpha	Epoxide hydrolase
JNK1 stress activated protein kinase	Farnesol receptor
NF-kappaB (p65)	Fatty acyl-CoA oxidase
Nitric oxide synthase-1, inducible	Glucose-regulated protein 58
Phospholipase A2	GOS24 (zinc finger transcriptional regulator)
Serum amyloid A1	Hepatic lipase
Serum amyloid A2-alpha	Lipoprotein lipase
Tumor necrosis factor associated factor 2 (TRAF2)	Liver fatty acid binding protein
Tumor necrosis factor receptor 1	Malic enzyme
Tumor necrosis factor receptor 2	Peroxisomal 3-ketoacyl-CoA thiolase 1
	Peroxisomal acyl-CoA oxidase
	Peroxisomal enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase
	Peroxisome assembly factor 1
	Peroxisome assembly factor 2
	Peroxisome biogenesis disorder protein-1
	Peroxisome proliferator activated receptor alpha
	Peroxisome proliferator activated receptor gamma
	Retinoid X receptor alpha
	Uncoupling protein 1
	Uncoupling protein 2
	Uncoupling protein 3
	Urate oxidase
	Very long-chain acyl-CoA dehydrogenase

TABLE 7

1-chloro-2-nitrobenzene	dt-5-fluorouracil
2,4-dinitrophenol	erythromycin
2-acetylaminofluorene	ethyl methanesulfonate
2-azido-2-deoxycytidine	etoposide
2-azido-2-deoxyuridine	fenofibrate
4-acetamidofluorene	flufenamic acid
5-azacytidine	gemfibrozil
5-chlorouracil	guanine
5-fluorouracil	hdp527
6-mercaptopurine	hydroxyurea
6-thioguanine	icrf
acetamidofluorene	icrf/doxorubicin
acetaminophen	indomethacin
acetylsalicylic acid	iodoacetamide
acridine	isonicotinic acid
actinomycin	M077
allyl alcohol	mechlorethamine
aminopterin	melatonin
aminotriazole	melphalan
antimycin a	methotrexate
antipyrine	methyl methanesulfonate
benz[a]pyrene	mitomycin c
bleomycin	mitoxantrone
busulfan	n-nitroso-n-ethylurea
caffeine	n-nitroso-n-methylurea
camptothecin	naloxone
carbamazepine	naproxen
carbon tetrachloride	nicotine
carboplatin	nitrofurantoin
carmustine	o-toluidine
chlorambucil	oligomycin
chloroquine	paclitaxel
cimetidine	PGU693
cisplatin	phenobarbital
clenbuterol	phorbol 12-myristate 13-acetate diester
clofibrate	prednisone
clozapine	proflavin
colchicine	progesterone
corticosterone	puromycin
cycloheximide	rezulin
cyclophosphamide	rifampicin
cyclosporin	rosiglitazone
cytosine arabinoside	sodium azide
dacarbazine	streptozotocin

dexamethasone  
diethylhexylphthalate  
diethylstilbestrol  
diflunisol  
digitoxin  
dimethylhydrazine  
dmso  
doxorubicin

tacrine  
tamoxifen  
thioguanine  
transplatin  
triethylenemelamine  
triethylenethiophosphoramide  
verapamil  
wy 14,643

**TABLE 8**

1	Activating transcription factor 4
2	Activin receptor type II
3	Ataxia telangiectasia
4	c-H-ras
5	c-jun
6	Carnitine palmitoyl-CoA transferase
7	complement component C3
8	Cytochrome P450 1A1
9	DNA dependent helicase
10	DNA mismatch repair protein (PMS2)
11	Epoxide hydrolase
12	ERCC 5 (excision repair protein)
13	ERCC 6 (excision repair protein)
14	Farnesol receptor
15	Gadd45
16	Glucose-6-phosphate dehydrogenase
17	Glutathione peroxidase
18	Histone 2B
19	Interleukin-1 alpha
20	Interleukin-6

**TABLE 9**

<b>CELL TYPES IN THE HEART:</b> Myocytes (cardiac muscle cells) Vascular endothelial cells Purkinje cells - regulate rate and rhythm of the heart
<b>CELL TYPES IN THE LUNG:</b> Columnar, ciliated epithelial cells - line trachea, bronchi, bronchioles Goblet cells - secrete mucus Neuroendocrine cells - contain serotonin, calcitonin and gastrin-releasing peptide Capillary endothelial cells Interstitial fibroblast cells Smooth muscle cells Mast cells - in pulmonary interstitium Type I alveolar (epithelial) cells - compose 90% of alveolar surface Type II alveolar (epithelial) cells - secrete surfactant and mediate repair of alveolar epithelium Alveolar macrophages Serous cells - produce a fluid to dissolve mucus Brush cells (Type III epithelial cells) Clara cells - highly metabolic Parenchymal cells (connective tissue cells)
<b>CELL TYPES IN THE KIDNEY:</b> Capillary endothelial cells Visceral epithelial cells (podocytes) - form glomerular barrier Parietal epithelial cells - line Bowman's space Mesangial cells - have contractile abilities to reduce amount of glomerular surface available for filtration Tubular epithelial cells Juxtaglomerular cells (modified granulated smooth muscle cells; also called granular cells) Lacis cells (non-granular cells) Fibroblast-like cells Macula densa cells (specialized tubular epithelial cells)
<b>CELL TYPES IN THE BRAIN:</b> Neurons Astrocytes - found in gray and white matter; responsible for repair and scar formation Oligodendrocytes - main component of white matter; produce and maintain CNS myelin Microglia cells - serve as macrophage-type cells Ependyma cells (columnar epithelial-like cells with a ciliated border) - line the ventricular system Fibroblasts Capillary endothelial cells Meningeal fibroblast cells Leptomeningeal (mesenchymal) cells Purkinje cells Meningothelial cells

**Macrophages****CELL TYPES IN THE LIVER:**

Kupfer cells - resident macrophages

Sinusoidal endothelial cells

Ito cells (lipocytes) - synthesize collagen and store vitamin A

Hepatocytes (parenchymal cells) - majority of cells in the liver are of this type

Bile duct epithelial cells

Hepatic venule endothelial cells

Sinusoidal epithelial cells

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
1	A + AP8	Inhibitor of apoptosis protein-1	310bp	AAGCTTTACCGCTGAGAATGATGAGGATGAAATGGTGGGGTGAAGGGTACATTAGGGAAATGGGAAACTTAATACAAAGAGATTATAAACAAATGTTAAAATTTGGCCAGGGAAAGAATTTGAAAGTTAGATAACATTAGGAATTTGGGGAAATAATTGTTCTAACCTTGAGGATGTGATGTTTCTCCTGGTAATGAGATGTCAGTGGCACTGGGCCACCTGGAAACAAAGCATGGATGCTGCAGTTGAAAAGGCCAACGTCTGTGAGATCAGGAAACCATGCTTGCAAACCACTGGTAAGCTTAACGAGGAAAAATATGAGTTAAATATTAGTTGACATTGTTGGAAACCAAGTTTAAACAATGANAAAAAAAGCAGGGGTGGGGTGGTCACTTGTGCTGTAAATCCCACACITGGAGGCTGAGGTGGGAGGATCACTTGAGGCAACATAGCCAGACCTCACTCTACTACATACTCTGAGCAATGCTAATCTGGCCCTTACTCCCTTAAGTCCTCTCTGGTAATAATGTTAAATCTCCAAATGGAGTACATTAACATTAAGCACCATTATCCAGCC	Repressed in Individual 1 and constitutive in Individual 2	AF070674
2	A + AP7	No significant match to anything	200bp		Repressed in Individual 1 and constitutive in Individual 2	AF261917
3	A + AP5	Gu protein (nucleolar RNA helicase recognized by autoimmune antibodies from a patient with watermelon stomach disease)	124bp		Repressed in Individual 1 and constitutive in Individual 2	AF261917

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
4	A + AP7	Ribosomal protein L34	117bp (65bp match)	GGAAAGCTTAACGAGGGCAGAAAAA TCGTTGTGAAAGTGTGGAAGGCAC AAGCACAGAGTCAGAAAAGCTAAAT AAAAAAATGAAACTTTTGAGTAA TAAAAATGAAAAGACGCTGT	Repressed in Individual 1 and constitutive in Individual 2	NM_000995
5	G + AP5	clone 459L-4 on chromosome 6p22.3-24.1	171bp	AAGCTTAGTAGGCCAAATAGGTTGT TGATGATGAAAGTGGTTGTGTTTA TAAGAGTCCTTATGGCTAGATGG CATTTGAACTTGGTGTCCAGTGT TACCAAGGACCCCTGAATTGAAAGAT ACATGCTGTGGCCCTTCAGCTCA GAAACTTTTACTTTCTATTGCC	Repressed in Individual 1 and constitutive in Individual 2	AL031120
6	C + AP6	eukaryotic translation initiation factor 3 (subunit 10 -theta)	126bp (86bp match)	AAGCTTGCACCATATCCACAGGAG TTGGAAAAAACATGCCATTCTCTG GAATTTAAGGGTGTGCATTATTC ATCAATCATTTGTGACAAAAAGA AAAACATAAAAATAAATTAAAATGT G	Repressed in Individual 1 and constitutive in Individual 2	NM_003750
7	G + AP7	ribosomal protein S9	94bp (86 bp match)	GTTAAAGGGCTGATCCTGTTATTTG GCAGGAAAACGAGACAAATCCAGCA GCCCGAGGGAGACAGGTGGACTT AAATCCCTCCCTCGTTAGCTT	Induced in Individual 1 and Individual 2	NM_001013
8	C + AP6		No significant match to anything	182bp	Repressed in Individual 1 and constitutive in Individual 2	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
9	C + AP7	No significant match to anything	98bp	CCAAGATGCCGGCACTGCACGG CTTTTATCAGTTTATTACATCAG GTCAAGGAAACAAATGGAATCTATC CACATGGTCTCGCTCGTTAACGCT AAGCTTAGTAGGCAGCACCTTAA AATATGTGAACTCAAATTGCAC TCCTTCAAGATGTTATCAATTGGTT ATGGTACTGTAGTTATAATAATT TGATTGAAACCCCTTAACAACCTCTT TGTTAAATTAACTCAATTAGTTGA TTTCAGTACTATTACATAGGAATT GATTTTATGGATATAGTGAAGAA ATGTGCTGTATTGGATAAAAATCCA CTTATTGTATGTGTGTAACTCT	Absent in Individual 1 and repressed in Individual 2	
10	G + AP6	KIAA1225 protein	252bp	AGATTACAACACATACAATAAGT GAATTTTATCAAATACAGCACATT TCITCTACTATATCCCATAAAAATCAA TTCCCTATGAAATAGTACTGAAAT CAAACAAAAATGAGTTAAAATTACA AAGAGTTGTTAAGGGTTCAATCA AAATTAAAAACTATAAGTACATAT AACCAATTGATAACATCTGAAAGA AGTGCAATTGGATTTGAGTTCACATATT TTTAAAGTGTGCTACTAAGCTT	Constitutive in Individual 1 and repressed in Individual 2	AB033051
11	A + AP5	erbB2-interacting protein ERBIN (KIAA1225 protein)	252bp		Repressed in Individual 1 and constitutive in Individual 2	NM_018695
12	G + AP7	angiotensin II receptor (AGTR1)	76bp	AAGCTTAACGGGGCTATCAGCAA CAAAGAGAAAGAGGCCAGGTCAAATGGT CTCAATAGCCAGGTCAAATGGT TGCCCC	Repressed in Individual 1 and Induced in Individual 2	AF245699
13						

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
14	C + AP11	Alpha-enolase	153bp	AAGCTTCGGTAATTGGCCCAAGT CATTGTTTTCTCGGCCCTACCTTCC ACCAAGTGTCTAGAGTCATGTGAG CCTCGTGTCAATCTCGGGGGGCC ACAGGCTAGATCCCCGGTGGTTT GTGCTCAAATAAAAAGCCTCAGT GACCCATG	Constitutively high in Individual 2 and induced in Individual 1	AF035286
14	C + AP11	Calmodulin 3	152bp	CAGGTAGTCACTGTATTATTGGAA AAACATTGATATATATTTCCTCAC AGCTTGAACTGAACACAATAATTGCC CGGTTAAAAAAACAAAAACAAAAA CATTCGGAAAATGTCCACAGGCCTC ACGCCCTACCTGCCCTAACCGAAG CTT	Constitutively high in Individual 2 and induced in Individual 1	NM_005184
15						
16						
17						
18	A + AP19	No significant match to anything	91bp	AAGCTTATCGCTCCCACTCCAGAG AAACCTTAATGCTCAGGGCTCAAAC TCCCTATCTTCCCTCCAGGGT CCTTCTGTCCCTTACT	Repressed in Individual 2, but not in Individual 1	
19						
20	A + AP19	Clone RG013F03	126bp (93 match)	AAGCTTATCGCTCGCAAGGGTTC CGTAGTTCTCTCGAGGCCATGCA TGCTTCTCATCATAGTAACGTACT ACTTGTAAATACATTTCTATTTC	Absent in Individual 2 and induced in Individual 1	AC005046

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
21	A + AP23	clone 1189B24 on chromosome Xq25-26.3.	289bp	ACTCTTGAAGATCTGTTAACATGATGATATAAAATTATTTCCCTCCAATCAAGAA-TATTATACATGACTTTAAAAAACATCATCAGTAGATAGACCGGAAGTTGATAATCGAAGTGGTAACTCTCACCGCCTGTGGAAACATGATCGCATAATCTCCCATATACTCCTGAAGGGAGAA-GATAAACCTTAACAACCTGGAAACATTAAAGTCCTTCAGCTGTAACCTCTGTCACTCTAGTCCTGTAATCACATTAAAATAATTGGTTAATCCATAGCCCAAGCCTT	Repressed in Individual 1 and constitutive in Individual 2	AL030996
22	C + AP22	Interferon, gamma-inducible protein 16	135 (71 match)	AAGCTTTGATCCTATGGAAATGGGTATTGGAGTGCTTTTAATTTTCATAGTTTTTTTAATAAAATGGCATTATTCGATCTACAACCTCTATAATTGGAAAAATAAAACATTATCTTTTGTG	Constitutive in Individual 2 and repressed in Individual 1	AF208043
23	C+AP17	Kinesin 1 (Kinesin receptor)	183bp	AAAGCTTACCAAGGTAGAGTGAAGTAATTGGAAACTGTTCAATTGAGGATAAAAAGGCATTGTATTATTTGGCAAATTAAGGCCCTTATTATTTTCACCCCTTCACTTGTCAAAACACTGAACAGAGTTGTCTTTTCTAATCCTTGTAGACTACTGATTAAAAGAGG	Constitutive in Individual 1 and repressed in Individual 2	NM_004986
24						
25	C + AP 24	KIAA0911 protein	119bp	CCAAACTAGTGGCATGTATAATAATGGCAGGATGGGGTACTGTGATGATTAACCTGACTTTTAATATTCTTGTGCTAGTGAAGCCTT	Constitutive in Individual 2 and induced in Individual 1	NM_014944

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
26	G + AP28	No insert - just vector sequence				
27						
28						
29						
30						
31	C + AP28	No insert - just vector sequence				
32	A + AP28	Ribosomal protein S12	80bp	ACATCACAAAGGCCAGGGTCTGT TATTAACCCCTCCAGCAGAG GGCAGTACAGTGTCTTGTC AGAAGCTT	Repressed in Individual 2 and constitutive in Individual 1	AF058761
33	C + AP27	KIAA0890 protein	69bp	CACAAGGGATAAAATGAACTTTATT TTAAATAAACATTGCACTCTGTAC ACAGCCCCAGCAGAACGCTT	Induced in Individual 3, but not in Individual 4	NM_014966
34	C + AP29	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit e (ATP5i)	149bp	CACACAACACAGGAAGCTTTATCA TCGGCTGCTGGTCCAAAGAGTGGG TCGCAGGGTCACTCACCTTAATATG CTGTCATCTCTGCCAATTCTCTGG CAATCGTTTCAGTTCATCCCTGCTT CTTCCTCTCTCTGCTGCTAAGCTT GGGCAGCAGAAATCAGGGTTATTGG AGGGATTGGGGTAGGGATGAGCAC GGCATGGGGCTTGAGGGTGTGG AGGGAGGCTCAGCAGGCCAGAAG CCCCCTTCACGGCAAAGTGGAA CCCGTGGTCATGCCACTTGGTCA CTCAGCAGAAAGAGGATGGGTC ACCAAGCTT	Repressed in Individual 3, but not in Individual 4	NM_007100
35	G + AP31	carbonyl reductase	175bp		Slightly induced in Individual 4, but not in Individual 3	NM_016286
36						

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
37	A + AP10	KIAA1224 protein	223bp	ACAGGTTTCATCTGAATACTATTTATTAGATAAAATTAGAGGGTGTCACTCATCTAACATACATAACGCTTCCAAGACTAGAAATCACAATTAGTTTGTGACCAGTTAAAGTATGAAATGATTGCATTGTACATACGATGTACAAAGACGATGATGGTTCTGTGGAGTTACTTCAGGCTGCACCTGGGGTGTGTTATGTGTGTACGTGAAGCG	Reduced in Individual 4 and constitutive in Individual 3	AB033050
38	G + AP11	CAMPATH-1 (CDw52) antigen	71bp	GCAAGTNCAAGGGTNACTTATTGACCCCCAGCTGGGACTGNTNGNC	Induced in Individual 4, constitutive in Individual 3	X62466
38	G + AP11	tumor necrosis factor type 2 receptor associated protein (TRAP3)	71bp	CCCTACATCAATTACCCGAAAGCTTGANATTGATGGTTAAATAACTCTGTCTTCGTGAGCTGGATGCCAAGCTTCTCACACTTACCCGAAGCIT	Induced in Individual 4, constitutive in Individual 3	NM_0211138
39						
40	G + AP10	Insert size doesn't match the autorad	54bp	AAGCTTCCACGTAACCAACAGGCCCTAAATCCATGATAAAGCTTCCACGTACTACC	Repressed in Individual 4, constitutive in Individual 3	
41	C + AP9	Sperm autoantigenic protein 17 (SPA17)	216bp (126 match)	CACAAACAGTAACGAATGTTATTCAACATCAAATCTCCCTCCTCAGGAAGAAATGACATTAATAAGAAGGTTGATGGATTGGATTATTTTCATGTTCTCTGGAGGTAAAACACAGTGTCTCACTTGTGTTTCTCTCCTCATTTGAAAGACTATTGTTTCATTTTCCGGATGAAAGCTT	Constitutive in Individual 3 and repressed in Individual 4	NM_017425
42	C + AP10	No insert - just vector sequence				

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
43	C+AP16	A kinase anchor protein 2 (PRKA2)	30 bp (matches 19)	CAATTATTGCCGGCTCTAAAGCTTC TGAAAT	Constitutive in Individual 4 and repressed in Individual 3	NM_007203
44	G + AP23	growth arrest specific transcript 5 gene	314bp	AAGCTGGCTATGGAGAGTGGCT TGACTACACTGTGTGGAGCAAGTT TTAAAGAAGCAAAGGACTCAGAATT CATGATTGAAGAAATGCAGGGTTT TAATGACCACAAACAAAGCAAGCATG CAGCTTACTGCTTGAAGGGCTT GCCTCACCCAAAGCTAGAGTCAGT GGCCTTTGAAGCTTACTACAGCCT CAAACCTCTGGGCTCAAGTGATCC TCAGGCCCTCCCAGTGGCTTTGTAG ACTGCCCTGATGGAGTCTCATGGCA CAAGAAGATTAAACAGTGCTCCA ATTTAAATAATTGCAATGCC AAGCTTATCGCTCAAAGTCTCCTAC CCTTCTCCCTCTTTAACGCCCTC TCTTCCTCGCTTTCTCTTACCTA GCTCCTTGTGGTGGCTGACTCTCTGT GCCTTAATCCTGTGACCCAGCCCC 45	Induced in Individual 4, but not in Individual 3	AF141346
45	G + AP19	5-aminolevulinic synthase 2 (ALAS2)	255bp	TTACACCACTTCCACCTTCCTGTC CGAAGTACACGGGACACTAGCTGCC CCAGGAAGTTGTGTGATTAAATC ACTTGTCTTGGCTGGAAAAGTGA TTTGTGATAAAATAAAGTCTGTGTA TTGGTTTC	Induced in Individual 4, but not in Individual 3	AF068624
46	G + AP23	Clone NH0523H20	101bp	GGGTGGAGGGGGTACTTTATGAAT ACCACAGGGACAAGGAAGGCTGC TCTTNTCACACACTGCTGAATCTCC GGATCTCGCAAGGTATAGCCAA GCTT	Constitutive in Individual 3, increased in Individual 4	AC005041

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
47		Very tiny insert				
48	G + AP23	Low molecular mass ubiquinone-binding protein	131bp	GCANACCATAGGAAGTTTATTGTGTCTTGANACACTACAATGCGAGCTCTCTCCANAGAAAGGTCTTCAAGACGGAACCGTCATCCGGATGCTTGCTCATTTGTCATAGCCAAGGCTT	Constitutive in Individual 3, increased in Individual 4	NM_014402
49	G + AP23	ATP synthase, H+ transporting, mitochondrial F1FO, subunit g (ATP5JG)	118bp	AAGCTTGCTATGATGTTGAAGACCAATCTTAAACATCTGATTATTTGATTATTATTTGAGTGTGTTGGACCATGTTGATCAGACTGCTATCTGAATAAAAATAAAGATTGTC	Repressed in Individual 3, but not in Individual 4	NM_006476
50	C + AP24	phosphoglycerate kinase 1	173bp	AAGCTTCACTANCACAATGTCGCCATGGACATTATCTAATTGTCCCCATCTCTCCACTGCTGCTGCCCACTCTTGCAATTCAAGCAATATANACATCTGATCCGGTTCTCAAGATTCTATTCTCACCCCTCCATAACAAAGTAGACAGG	Induced in Individual 4, but not in Individual 3	S75476
51	A + AP23	Acid phosphatase 1	274bp	ATATCTCTAGTTGTTATTTATACTCCCCAGTTTATTGAAATATTGATTTGACATTATCTCAAAATACACAGAAATTACCTTACATCTGCCATTACATTATTAAATGCTGTGATGAAGAA TACTTATTCAATATTAGCATGCCAAATAATAACACTTCCCAACTTTAAAATTATTAAAGCCAAATTATGGACATTGGGTACATGTGCATAAAAAACAGTCATATTCTCAACTGACCATAGCCAAAGCTT	Constitutive in Individual 3, repressed in Individual 4	NM_007099

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
52	C + AP20	Clathrin, heavy polypeptide-like 2 (CLTCL2)	246bp	CCACAGTCCAGTAATTATTTAAA TTTGAGTAATTCAAATTCCACAAA CAAACGTAAAGAACAGCAATTATTT GTTGAATTTCCTCTCTGTACAC TCAGTGATCTAAACACCACAATAT CCAACATACACAAACCTCAGGGAA GGTTAGTAACACACACAAGATT GGAAATCATGGTGCCTTTGCTCCT GAATGGAATGGTCCCACAGAAAAA GCACAGGATAACAGCACAAACAGCT T	Induced in Individual 3, repressed in Individual 4	NM_004859
53	C + AP21	MHC class II HLA-DR-beta (DR2-DQw1/DR4 DQw3)	223bp	AAGCTTCTCTGGACCTGGTGCTA CTGGTTGGCAACTGCAGAAAATG TCCTCCCTGGTGGCTCTCAGCT CCTGCCCTGGCCCTGAAGTCCCAG CATTGATGGCAGGGCCTCATCTTC AACTTTNGTGCTCCCCCTTGCCCTAA ACCGNATGGCTCCCGTGCATNTG TATTCAACCTGTATGACAACACAT TACATTAAATGTTCTCAAAGAT GG	Repressed in Individual 3, but not in Individual 4	M20430
54	A + AP23	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex	250bp	AAGCTGGCTATGGTTAAAGGGGA ACCAGATGTTAAAAAATTAGAAGAC CAACTCAAGGGGGTCAATTAGAA GAGGTGATTCTTCAGGCTGAACAT GAACTAAATCTGGCAAGAAAATGA GGGAATGAAACTATGGGAGCCAT TAGTGGAAAGGCCCCTGGCGATC AGTGGAAATGGCCAATAATTATT AAGTGACTTTGGTGTTCATGGG AAACTGATGTAATTAAATATTCTGTT ATATT	Constitutive in Individual 3 and repressed in Individual 4	NM_005000

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
55	C + AP19	clone 717M23 on chromosome 20	363bp	CCAAATTTCACATTATTGAGTTA CCACCAAAAGTGTAAATTAAACAT GTGATAGAGGTTGACAGTAGGTT CATTAGTACAACATGCCTATGTTT TATAAAATTAGCTGATCAACTA GAGATAAAATAATTACATTACGCTT TTAGGTCCTTTACATTACGCTT CTTCACAGGGTGGAAAAAACAAACC GGAATTGAGAAGCTCCCTACTGGC TGGTATCCATTGGCAGCTGCCTGC CAGAAGTAGGAGACAGCTGCTCC ATCCAAGACACGTCTCCTCATCAC TGTTGAGGGAAATCCCACACTGTGGT CGAGCGATAAGCTT	Induced in Individual 3 and repressed in Individual 4	AL050321
56	C + AP20	FLJ22624 fs, clone HS105951	85bp	AAGCTTGTGTGTCACAGGGATC ATGATGGTGACTGGAAAAATTAA CTTCAGTAACATGCTTAGCTTCC CTCCCTTAATGTG	Repressed in Individual 4, but not in Individual 3	AK026277
57	C + AP24	No significant match to anything	106bp	AGGGTTTACCAAGAGCATTATT TACTCTTAAGATACTAATGAAGAC CCTTAATTTGGTAAAATCATAACA TATAGGTACATTACAGCTAGNG AAGCTT	Induced in Individual 4, but not in Individual 3	
58	C + AP19	clone RP11-468G5	72bp	AAGCTTATCGCTCAATTAGTCATT AACAGAAAACTCTACAGGATTATAACA CACAGTAGTAACACTGGCTTG	Induced in Individual 4, but not in Individual 3	AC009238
59	G + AP2	histone macroH2A1.2 (H2AF12M)	31bp	AAGCTTGCACCATGTACCCCCACT TCAGTTT	Increased in Individual 3, not in Individual 4	NM_004893

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
61	G + AP3	KIAA0949 protein	104bp	AAGCTTACGAGGAATGAGAACAC AAGGAATGATTCAAGATCCACCTTG AGAGGAATGAACTTTGGTTGTGAAC AATTAGTAAAATAAGCAATGATCT AAACT	Repressed in Individual 3, but induced in Individual 4	AB023166
62						
63						
64						
65						
66						
67	G + AP5	BCL2-related protein A1 (BCL2A1)	122bp	CGAGAAAAATACATACAATTATTTC ATTACATGGGGACAAAAATTCCATA ACTCTGGAAAGGTCAAGTTACATCAT CAAAGTGTTTATTAAAAGTAGAA GTATGTTGGCAATCAAGCTT	Increased in Individual 4, but not in Individual 3	NM_004049
68		Insert is too small				
69	A + AP4	No significant match to anything	139bp	CACAATTATTATTGAGCTTTGCT GTATGTTAGCTTTGGAAAGTAGATT TATAGTTAGAATTGTTGCCTTCC TTTTTAATCTTTCACTCTTCATT ATTGAGCTATGAATTAACTATTGTA GGGGTAAAGCTT	Induced in Individual 4, but not in Individual 3	
70	A + AP4	chromosome 21, clone:KB51A8	123bp	AAGCTTACCGCTACTGAGTCTGT GTAGTAAATTGGACTAGGNACAT GGTGAGATTACATTAAAGTGTG AAGTTTGTAAAGGTTCCTTAAAG AAATTACGCCTTCTGGCGGGCG	Slightly Induced in Individual 3, but not in Individual 4	AP001628
71	A + AP3	No significant match to anything	110bp	AAGCTTAAACGAGGGATGGCAGCTG ATGGGTACCGGTTCCCTTATGGG ATGATGAAAAAGCTCTGAAATTAGC TGTGGTGTGATAATTGACAACTC CGTGGATATAAG	Induced in Individual 4, but not in Individual 3	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
72	A + AP3	RECQL4 helicase	50bp	CCAAAGTGGAGTTTATTCTGC ATTTGGAGCCTCGTTAAGCTT	Induced in Individual 3, but not in Individual 4	AB026546
73	G + AP4	Insert is too small			Induced in Individual 4, but not in Individual 3	
74						
75						
76	A + AP23	cyclin D2	179bp	AGGTCAGGGGAGTTATTGTCCA AATAGCATAACCTAAATTGCATTCAA AACCATTTCAAAATCCATCCTTTAA CTAGTCANAAAACAGGGTTATTATT TTTTAAATCAGCTTANCACTGAACAG ATAAGACCTCTTAAAGGCAGCTG ACTATATCATGTGACCATCATAGCC AAGCTT	Highly induced in Individual 4, but not in Individual 3 or Individual 5	NM_001759
77	A + AP23	clone RP1-83P18 on chromosome 1	124bp	AAGCTGGCTATGGGTTGCCTAA TTGATGTTTGAGGAAGCATATTAA TGTATAAACCTTCGCTGACTTTGAA GGTNGTGTGTAGCATGAGGGANCA CAAATAAAACAATTCTAAATCAAAC T	Induced in Individual 4, but not in Individual 3 or Individual 5	AL356379
78	C + AP19	No significant match to anything	38bp	CTAGAAAAGAGACACTCCATAACC TGAGCGATAAGCTT	Induced in Individual 4 and Individual 5, but not in Individual 3	
79	C + AP19	No significant match to anything	36bp	AAGCTTATCGNTCAGGTATGGAG TGTCTGCTTCT	Induced in Individual 4 and Individual 5, but not in Individual 3	

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
80	C + AP24	cytochrome c oxidase subunit VIic (COX7C)	213bp	CACGTCATTAAGTTATTGACAAACA TATCTAGTATGGCATATGAGTTCTA GTTTGATGCCACTCCAGGGCTGC ACCTCTAAATGCTCTTCATATCT GTAAATGGAGGAACCTGAAACATC CTTATGTTTAAGCAGTTGGTGTCT TACTACAAGGAAGGGTAGCAA TGCGAGATCCAAGTACAAACACATC TTAGCTAGTGAAGCTT	Induced in Individual 3, but not in Individual 4 or Individual 5	NM_001867
81						
82	C + AP24	clone RP11-358M9	146bp	CAGTTAAAAGAAATGGTAGACAC CTATAATTACTTTGTTAGACATACA AAGGCTAGCCCTTTGACTTGTAC AAAGTTTCAAACTTTCATATACAA ATATGCCACTATTCTATTCA TCGGACAGCTAGTGAAGCTT	Very high expression in Individual 4 and Individual 5, but not in Individual 3	AC020595
83	C + AP19	Human mitochondrial DNA	35bp	AAGCTTATGGCTCACACCTCATATC CTCCCCTACTG	High expression in Individual 3, but not in Individual 4 or Individual 5	NC_001807
84	C + AP1	ribosomal protein L3	64bp	AAGCTTGATTGCCAGAACAGATT TGCAGTTGGGGTCTCAATAAA AGTTATTCTTCCACTG	Slightly induced in Individual 3, but not in Individual 4 or Individual 5	M90054

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
85	C + AP8	No significant match to anything	239bp	AAGCTTTACCGCTAAAATGATGAT ACANGTTGAAGACACATCACTCTG AAATTGGAAAGACCTCAACCTAAAG GCTCCACAGTGGCTTACTCAGCTG AACTCTAGTTACTACTCTTACTT TGTCNACCCATGGGGGTGCAGT TTTTTAAATGTTGGAGATGCC ATTCTAACACTACTGTTGAATGTCTCT GTTTGGGGAGGTATAACAAGAAAT AAAAAGANTATATG	Induced in Individual 4, but not in Individual 3 or Individual 5	M35543
86	C + AP19	GTP-binding protein G25K	266bp	AAGCTTATCGCTCCAAAGACTGCT GAAAAGCTGGCCCGTGAACCTGAAG GCTGTCAAGTATGTTGAGGTCTTCT GCACCTTACACAGAGGGTCTGAAG ATATGTTGATGAGGGCTATCCTAG CTGCCCTCGAGCCTCGGGAAACTC AACCCAAAAGGAAGTGTGTNTATT CTAAACTGTTTCTCCTCCCTCT TGCTGCTGCTCCCTGTCCCCACTA CTGNAGAAAGATGTTAAAAACAA AGGAATAAAACCNCTCGTTG	Induced in Individual 3, but not in Individual 4 or Individual 5	

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
87	C + AP36	ribosomal protein S4, X-linked (RPS4X)	332bp	AAGCTTCGACGCTGGTAACCTGTG TATGGTGACTGGAGGTGCTAACCT AGGAAGAATTGGTGTGATCACCAA CAGAGNGAGGCACCCCTGGATCCTT TGACGTGTTCACGTGAAAGATGC CAATGGCAACAGCTTGCACACTCG ACTTTCACAAACATTTTGTATTGGC AAGGGCAACAAACCATGGATTCT CTTCCCCGAGGAAAGGGTATCGC CTCACCAATTGCTGAAGAGAGAGAC AAAAGACTGGGGGCCAAACAAGAC AGTGGGTAAATGGTCCCTGGT GACATGTCAAATCTTGTACGTAA TAAAAATAATTGGCAGG	Slightly induced in Individual 3, but not Individual 4 or Individual 5	NM_001007
88	G + AP1	clone RP1-68D18 on chromosome 11p12-13	231bp	GGTCAAGACACCTTCAGAAAAATG TTAGAATCTACACCTACGTTCAGTC TTTCATTGTGTTCAACATTGGCTAA TCATTTTTATCTCTCTAGTATCA GATCAGATCAGTGTACCTCCAAAC AGAGATGGAAGCTACACTGCAGTT CCCAATACTACTTCAGCATAGGCA AAAATGTGAAGCCAAATTAAACAGAGA AATCATTGGCATTATTAGGCAA TCAAGCTT	Very high expression in Individual 4 and Individual 5, but not in Individual 3	AL133330
89	G + AP36	Human mitochondrial DNA	28bp	GCGGGGGGGGATATGGGTCGA AGCTT	Induced in Individual 5, but not in Individual 3 or Individual 4	NC_001807
90						

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
91	C + AP39	ecto-ATP diphosphohydrolase	113bp	AAGCTTCCAGCTACACCTTCTCCTTGACTTTGTGCTTAGGT TTAAAGACCTGACACCTTCATAA TCCTTGCTTATAAAAAGAACATTATT GACTTTGTCTAG	Induced in Individual 3, but not in Individual 4 or Individual 5	AJ133133
92	C +AP3	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 9kD (ATP6H)	131bp	AAGCTTGGTCAGTAGGAGAGCAC GTTCAGAGGAAGAGCCATCTCAA CAGAATCGACCAAAACTATACTTCC AGGATGAATTCTCTTCTGCCAT CTTTGGATAAATTTCTCCTT TCTATGG	Induced in Individual 3, but not in Individual 4 or Individual 5	NM_003945
93	A + AP3	cyclin D2	265bp	AGTCAAGGTGAGTTATTGTC ATAGCATAACTTAATTGCATTCAA ACCATTTCAAATCCATCTTTAAC TAGTCAGAAAAACAGGGTTATTATT TTAAATCCTTAACACTGAACAGA TAAGACCTCTAAAGGCAGCTGA CTATCATGTCAACATAGC ATACAACATTGGCATAACTCTCT ATGCTACTTATCAGCAGCTTCTAAC ATCCTGACCAAGCTT	Induced in Individual 4, but not Individual 3 or Individual 5	NM_001759
94		no insert - just vector				
95		No significant match to anything	122bp	AAGCTTCGACGGCTGGGACACCAA GAACAGAGAAAGTAAAGATTAAAGT GTTCTGACATTTCCTACAAATGATCT TGGCTTCTGACCAATTGTTTCT CCTACCAAGTACTTGCTCAGTGT	Induced in Individual 1, but not in Individual 6 or Individual 7	
96						

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
97	A + AP8	Inhibitor of apoptosis protein-1 (MIHC)	310bp	<pre> ACCAGNNGTTGCCAAGCATGGTTT CCTGGATCTNACAGACGTTGGGCT TTCAACTGCAGACTTCATGCCTT GTTCCAGGTGGCAGGAAACAT CACATCTCATTACCAACAATTATT CCCTCAAAGGTAAAGTAATTGTATCT AACTTCAAATTCCTTCCCTGGCC AAAAATTTCACACATTGTTAAAAAA TCTTCTTGTATTCACTCACTGCTTT ATATTAATTCTAAGTTCTTCATT TCCTAAAATGTAACCTCAACCAAC ATTCTCATCCTCATCATTCTAGCG GTAAGGCTT </pre>	Induced in Individual 7, but not Individual 6	AF070674
98	A + AP8	ribosomal protein L35a (RPL35A)	441bp	<pre> ACAAGAGCACAATCCACATTATT TATTGATTTTTCGTTAGTTAACATCC TTGAGGGGTACAGCATCACTGGGA TTCTGTGTCCTAACGGCCTTAGCAG GAAGATTGCTTCGGAATTGGCAC GAACCATGCCACTGTTCCATGGG CCCGAGTTACTTTCCCAGATGA CTCTGGTTGGTTGGTTGGGCC AGGAGTTGACTGTGTTGTTCTTGCT TTATATACATAAGGCATCTCTGC CCAAATAGAAATTCTGTTCATCTCG GGCGTAACACCTCAATTAAAGA AGAGCTGTGTGCTCCCTTGGTT CGGAGACCCCGCTTATAGCCAGCA AAAATGGCCCTGGACACAGCCTT CCAGAGATAAGTCCCTTTAGAAAGT CCGTTCCAGCAGGGCTCCACAG GAGCCAAGATGGGGTAAAGCTT </pre>	Induced in Individual 7 and not in Individual 6	NM_000996

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
99	G + AP10	ribosomal protein S12	443bp	AAGCTTCCACCGTAACCCACCGCCA TGGCCGAGGAAGGCATTGCTGCTG GAGGTGTAATGGACGTTAATCTG CTTTACAGGAGGGTTCTGAAGACTG CCCTCATCACCGATGCCCTAGCAC GTGGAATTGCGAAGCTGCCAAAG CCTTAGACAAGGCCAACGCCCCATC TTTGTGTGCTTGCACTCCAACGTGTA TGAGGCCTATGTATGTCAGTTGGT GGAGGGCCCTTGTGCTGAACACCA AATCAACCTAATTAGGTGATGAC ACAAGAAACTAGGGAGAATGGGTA GCCCTTGTAAAATTGACAGAGAG GGGAAACCCCGTAAGTGGTTGT TGCAGTTGTGTAGTAATTAGGACT ATGGCAAGGAGTCTCACGCCAAGG ATGTCATTGAAGAGTATTCAAATG CAAGAAATGAAGAAATAATCTTG GCTCAC	Very high expression In Individual 1 and Individual 7, but not Individual 6	NM_001016
100	G + AP10	Thymidylate synthetase	198bp	GCAGAACACITCTTTATAGCAA CATATAAAACCAACTATAAAAGTTCAT AACCAACACTACATCATGATCGAT GGTGTACTCAAGCTCCCTCAGATT NGAGGGAAATAGCTNGTGAATTCT TAAAATATTCTAAAAATATTCCAAA ATAGCTNGTGAATNCACCAACCTT CTTTATAAGTACGTGAAAGCTT	High expression in Individual 6, but not in Individual 1 and Individual 7	NM_001071

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
101	G + AP12	chromosome 17, clone hCIT.211_P_7	314bp	GGAAAGTAGTATTTCATTTTATTAT AAGGCAGTGCTCCCAAACCTTTCAC AGCGGTACACCTNGAGGTTGGATGGGG CATCCCAACCNACCTGGATGGTAACCT GATGGAGGAAGCTCTAGTGTANAAA TTCAGGGACCGAACCTGGTCTCAAAGCAG AGGGCTTGTTCAAGTCCCTGTTC TGCCCACTTACTAACTGCATGACCTT GAGCAAGCCACCTTAATTCTCTGCT CCTTCTGTGAAATGGGTACAATG TGGTCAGCAGTAAAGGAACATAA CACGTACAGCACTCAAGCTT	Higher expression in Individual 1 and Individual 7 than in Individual 6	AC003665
102	G + AP19					
103	G + AP19	just vector				
104	A + AP3	cyclin D2	265bp	AAGCTTTGGTCAGGATGTTAAAAG TGCTGATAAGTAGCATGATCAGTGT ATGCAGAAAGGTTTAGGAAGTAT GCAAAATGGTTATGGCTATGA TGGTGACATGATATAGTCAGCTGC CTTTTAAGGGTCTTATCTGTTCA TGTAAAGTGAATTAAAAATAATA CCTGTTCTGACTAGTTAAAGAT GATTGAAAATGGTTGAATGCA ATTAGGTTATGCTATTGGACAATA AACTCACCTGACCT	Induced in Individual 1, but not in Individual 6	NM_001759
105						
106		just vector				
107		just vector				

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
108	C + AP16	clone DKFZp564O092	355bp	AAGCTTTAGGGTCAGTAAGCGA GAGAAAGGACGGCAAAACGAGCA ATGTCACTAGCTCACAAACTTCAATT CCCTTACACACACTTAGCATCAG TGCTTTGACAGGGGAACCTGTTCA TCTTGATGAGGATCAGAACCTCATT AGAAGGCCGAAGAAGATAACCTCAG AAAGGTCGGAAAGAAAAGGTTT CGGAGGGGGGTGATTATGGGT GTACATATTGTATATTTCATGGTCA CCTGAGATACTTCTAAATTTCATTGT ATATAGGGTTTCCCTGGAAATT ATTAATTGGTTGGCTTGGACATGTG GAAAGGCCCTACTAATAAAATTGA TTTACTTATG	Strongly induced in Individual 1 and not in Individual 6	AL050003
109	C + AP9	cDNA FLJ11508 f1s, clone HEMBA1002162	150bp	CCATCAAATGTAATTATTTAAATAA CAATTCAATTGCAATGTTAAGTAAAC CAGTTGAGCAATATAAAAATACAG AATTTGGAGAAAATCTGGCAAAATT AACCTGTATCTAAATGCAGCATATT CTGTGATACTACGGATGAAGCTT	Slightly induced in Individual 1 and not in Individual 6	AK021570
110	A + AP22	mitochondrial genomic DNA	64bp	AAGCTTTGATCCAAGCCTACGTT TCACACTCTAGTAAGCCTCTACT GCACGACAACACAT	High expression in Individual 6, but not in Individual 1 or Individual 7	NC_001807
111	A + AP20	NADH dehydrogenase-ubiquinone Fe-S protein 2 precursor	69bp	AAGCTTGGTGTGCATGTAACAAAAA AGGAGAAATTATAATAATTAGCCG TCTTGGCCCCCTAGGCCT	High expression in Individual 6, but not in Individual 1 or Individual 7	AF013160

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
112	C + AP9	No significant match to anything	165bp	AAGCTTCATTCCGGGGTACCGTTAGGGCTCTTATTGACCATTCTGAA CAGCGTGTCTCTTCTTGGTTCTTGTTGTTCAACCTCTTAA AAGTTTCTCTGGCTAACCTCTTAAATGAAAACCTTGG CTTTCCGTTCCAACCTTCCCTCTGG GCATGGCTCTTTGG	Induced in Individual 1, but not in Individual 6 or Individual 7	
113	C + AP9	cytochrome b gene	233bp	AAGCTTCATTCCGATAAAATCACCT TCCACCCCTTAATGACATAACAAAGA CGCCCTCGGCTTACTACACAATCAAAGA CTCTCCTTAATGACATAACACTAT TCTCACCAGACCTCTAGGGGACCC CAGACAATTATAACCCCTAGGCCAAC CCTTAAACACCCCTCCCCACATCA AGCCGAATGATAATTTCCTATTGCG CTACACAAATTCTCCGATCCGCCCC AACAAACTAGG	Induced in Individual 1, but not in Individual 6	AF254896
114	C + AP11	just vector				
115	C + AP10	lysosomal peptidase insensitive protease (CLN2)	157bp	AAGCTTCACGTAGTATTGAAATGG CCAGTTTACCTGTCCTGCCCTCTT CCAAGACCGTTGGCTAGAGGA CTAGAACATGTCCTATTAACTTT GTGTTCCAGGTCCTAGCTCAGGA GTTGGCAAATAAGAAATTAAATGCT GCTACACCG	Expression In Individual 6, but not in Individual 1 or Individual 7	AF039704
116	C + AP19	clone 108K11 on chromosome 6p21	52bp	CAAACAAATTCTTACCTCATTC TGTTCTCATGTTGAGCGATAAGC TT	Induced in Individual 7, but not in Individual 6	285986
117	C + AP19	No significant match to anything	117bp	AAGCTTCATCGCTCACACTGT TGAATTAACTGTGGCTTGTAAA ACAAGAAGGAATGAATTATACTGA AGTAAAGTCCTGAGTTATGCCCA AATGAGATGACCCCTGG	Induced in Individual 1, but not in Individual 6	

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
118	C + AP19	No significant match to anything	213bp	CTAGGTCTCTTCCAGTCCTTCTAC CTCTTCTAAACTGAAATCTCTCAAAA GCCCTCCTGCTCATCTCTGAGTGGTT ACTGGCTGACCTTCCAAACCTTCCA ATGAACGGAGGTGGAAAATGGTAA ACTGGAGGTAATGAGGAAGGGTCA CAACTGGAAATTCAACTTAGGATCAG AGAAATCAAATCTTGAAAGCAGTTTC AACTTGCTTATATCTT AAGCTTGGCTATGGAAAGAATGAAAT AGCAAAAAAGGAGAATTTTTAA AAAGATCTCTCACTGGG	Repressed in Individual 6, but induced in Suzanne	
119	C + AP23	No significant match to anything	66bp	CAACATCACCAAAATAATTATTTGG ACTCGAGAAATTAAAAGAACATTGAC AGTTATGAAATGCATGTTTATTCTG AAACTCTTAACTAGTTGTACAACATA ATCCGTGACAAATTACCGAGATAATT TTTACTTTATTTCTTCAGGCCTGG GTTTTTCGATGACTTCAAATTGGG ATCTTCATAATTGAAAGTGGAAAT TTGCTTGAAGCTTAAACAAAGCTCCCT GTATTCAATGCTGCATTACCAAACA TTGCTTGAAGCTTAAACAAAGCTCCCT CTCCAGCTCTGCTGATACTCTGAA CTAGGCATCAACAGGTCTCCAGAT GTCCTGCGCTTAGATTGTATTCTC TAATCTTGTCCACAAAGAGTTCTG TATAGGATCAAAGCTT	High expression in Individual 6, but not in Individual 1 or Individual 7	M37104
120	C + AP22	mitochondrial ATPase coupling factor 6 subunit (ATP5A)	366bp		Induced in Individual 7, but not Individual 6	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
121	C + AP19	clone 717M23 on chromosome 20	363bp	CCAATTTCCTCAATTATTGAGTT CCACCAAAAGGTAAATTAAACAT GTGATAGAGGTGACAGTACGTT CATTAGTACAAACATGCCATAGTT TATAAAATTATAGCTGATCAACTA GAGAATAATAATTATCCTTTAT TTAGGTCTCTTTACATTACAGTT CTTCACAGGGGGAAAAAACAAACC TTCACACAGGAATTGACAATCAA GGAATTGAGAAGGCTCCCTACTGGC TGGTATCCATTGGCAGCTGGCA CAGAAGTAGGACAGCTGCTCCTC ATCCAAGACACGTCCTTCATCAC TGTTGAGGGAAATCCCACACTGGT CGAGCGATAAGCTT	Gene expressed at same level in everyone	AL_050321
122	C + AP19	clone RG013F03	126bp	CGAAAATAGAAAAATGTTTACAA GTAGTACGTTACTATGATGAGAAAG CACAAAGACACCTGCTGCTATAATA CATGCATTGGCTCGAGAGAAACT ACGGAACACCTGAGGCGATAAG CTT	Repressed in Individual 1, but not in Individual 6	AC005046
123		Just vector				
124	G + AP10	thymidylate synthetase	196bp	GCAGAACACTCTTATTAGCAA CATATAAAACAACTATAAAGTCAT AACCACACTCTACATGATCGAT GGTGTACTAGCTCCCTCAGATT GAGGGAAATAGCTGTGAAATTCTTA AAATATTCTAAAATATTCCAAAAT AGCTTGTGAAATTCAACCAACCTCT TTATAAGTACGTGGAAGCTT	High expression in Individual 8 and Individual 4, but not Individual 9	NM_001071

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
125	G + AP19	clone RG013F03	126bp	AAGCTTATCGCTCGAGGGTGTCCGTTAGTTCTCGAGCCAATGCA TGTTATTAGCAGCAGGTGCTTGCCTTCATAGTAACGTACT ACTTGTAATAACATTTCTATTTTC	High induction in Individual 4, but not in Individual 9	AC005046
126	G + AP19	clone RG013F03	126bp	GGAAAATAGAAAAATGTATTACAA GTAGTAGCTTACTATGATGAGAAAG CACAAAGAACACCTGCTGCTATAATA CATGCATTGGCTCGAGAAGAGACT ACGGAACACCCCTGGAGGCATAAG CTT	High induction in Individual 4, but not in Individual 9	AC005046
127		just vector				
128	C + AP9	clone YB26B05	276bp	CAGGAGGCATGCAGGGAGCAC TGCAAGATGATCAAAGTTTTATTAA CATTATAAGAACACTAAAAATAAAC AATATGATTGCAATTCTGTGTGA ACTTGAAAAAATGTGTTCAAGCACA CATAAAAGCAACAAGTTTACCCCC AACAAAGTATGCTATGCAAGCCAGTC CCTAAACTGCTGGGGTAGCAGCACTGC TCTCAACAGACAGCTGGGTAGGA GGTAGGCTGCTGGTGCCCTGAG GCAGGTGGCTTTCCCTACTCGGAA TGAAAGCTT	Repressed in Individual 8 and Individual 4, but not Individual 9	AF147336

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
128	C + AP9	uncoupling protein-2 (UCP2)	267bp	AAGCTTCATTCGGCTCCTTACCTA CCACCTCCCTCTTCCCCACCT TCCTTCCGTCCTTACCTACCC TCCCCTCTTCTACATTCTCATCTA CTCATTGGTCACTAGTGCTGGGAG TTGACATTGACAGTGTTGGAGGC CTCGTACCAGCCAGGATCCAAAGC GTCCCCGTCCCTGGAAAGTTCAAG CAGAATCTTGGTCTGCCCGAC AGCCCAGCCTAGCCCACCTGTCA CCATAAACGCAAGCTAACCTGG	Repressed in Individual 8 and Individual 4, but not Individual 9	AF096289
129	C + AP16	Cide-b (CIIIndividual 3)	385bp	AAGCTTTAGAGCGGGGGTAGCA GTCACCTGAGTAAGTCACTGGGT TCAGAGCTGAGGGTACTCCATGG TGGACCGGAGGTTCTCCCTGG AACTTCTGGCTGGGGCTTAGTGGT CCTGTGCTGGGGCTTAGTGGT TTCTGTGTTACAACCTGGATCTCA GCCAGGACAAGGTGGGAATGAGT CAAGGCCTGGACTCTGCCCTCG CCTGGCCAGTAAGAAGGGCAAAGT CCAAGGGAGGGATGAGGGAGGG GCCAGAGATGGGGTCTGGAGGAAG AATTGGCCTGGAAAAGCCATTGGA GCTTGTATGTTGTTGGTAGATGG ACATGTTGTTGGAGGATGAAATGTG AACCATGTAAGGATGAAATGTG	Induced in Individual 9, but no in Individual 8 or Individual 4	AF218586

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
129	C + AP16	No significant match to anything	385bp	CTGGGAATAAAACTACATCTCAAAA CCTCTTTGCAACCGAGTTGTGAGTA TGTTTTACCAATAAGACATAAGCA GATAGGGATGCAAGTCACCTCCCT AACAAACATCTTATAAGCCAGCTG ACACATACCCATTCAACCATATCATA GGTTATGTAGTCTCAGGTTGCTGC AGAGTAATGTCCCTCTTAGACATG GTAGAGAATTATGTACAGTGGAG CAGAGACTGAGCAACTACAGACT TCAGGCCACATAACTTACTCTCTAT TATAAGACAGCAAGAAAACAGACTT ATCTCCAGAGTCACACAGCTGGT ATCCAGAGAAGGGAGAAAGGGATAC AAGTATGTGCACTCTGAATATGAAC ACTACGCTCTAAAGCTT	Induced in Individual 9, but not in Individual 8 or Individual 4	AJ230610
130	G + AP43	mitochondrial DNA for D loop	230bp	GGGTATGCAAGCGATAGCATTGG AGACGCTGGAGCGGGAGCACCC ATGTCGCAGTATCTGTCCTTGATTC CTGCCCTCATCCTTATTATTCGCA CCTACGTTCAATATTACAGGGAAC ATACTTACTAAAGTGTGTTAATTAT TAATGCTTGTAGGACATAATAATA CAATTGAATGCTGCACAGCCGCT TTCCACACGACATCATAAACAAAA ATTCCAC	Induced in Individual 1, but not in Individual 6	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
130	G + AP43	no significant match to anything	260bp	GAAATTGGATTAAATTCTTATATC ATTCTGCAACTTTCCATGCTTT GAAATTATTAAAGAAAGTTAACAAA TAAGCAAACAAACTAACAAATCAGGA ATGAAAGTGAAATTACAAAATGC CATTTCAGATTACAAGACGCTTGC CATTACACCGCTATGATTCTCT CCTTTTCCACACACACACGGCTCCA GGTCTACTTGCTTACTCTCCCCG CTTCAAGCTT	Induced in Individual 1, but not in Individual 6	
131						
132						
133		No insert - just vector				
134	G + AP47	chromosome 10 clone RP11-70E21	257bp	GAGATAGAGCTCTGGCTGATCACCT AGGTGGAGTGCAGTGGCATGATGTC ATAGCTCACTGCGGGCTCAAACCTC TTAGGTTCAAGATGATTCTCCACCT CAGGCCCTCTGAGTAGCTGAGATTA TAATTTTTTTGTAAGATGGGG TCTTGTCTATGTTGACTATGCTGGC CTCAACCTCCTGGCCTCAAGTAAT CCTCCTGCCCTGGCTTCTGGAAATT ACGGGCATAAGCTT	Induced in Individual 1, but not in Individual 6	AC016399
135	A + AP41	matches a bunch of sequences that make no sense	158bp		Induced in Individual 1, but not in Individual 6	

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
136		Jun B proto-oncogene (JUNB)	112bp	ACTTAAATAGATTCAATAAAAAGAA CAAACACACACACAAAAACACAAACACG TCTTAAATAAAACTCTTTANAGACT AAGTGCGTGTTCCTTCCACAGTA CGGTGCAAAAGCTT	Induced in Individual 1, but not in Individual 6 or Individual 7	NM_002229
137		Chromosome X clone bWXD501	63bp	ATAAAGAACCAAAAGAAATTATT ACAAATTCTTACTTGACCAAGTT GTCAGGCCAAGCTT	Induced in Individual 1, but not in Individual 6	AC004677
138		No insert - just vector				
139	A + AP47	Chromosome 16 BAC clone CIT987SK-A-67A1	106bp	AGATATGAAAGTCCCACTAGGTG CCCTGGCTGGCTTAACACTCTGG TTTCAAGTGTATCCTCCTGCCTGG CCTTCCAAATGCTGGTATTACGG GCATAAGCTT	Induced in Individual 7, but not in Individual 6	AC004531
140	A + AP47	Chromosome 16 BAC clone CIT987SK-A-67A1	106bp	AAGCTTATGCCGTATAACCAGCAT TTTGGAAAGGCCAAGGCCAGGGAT CACTGAAACCAAGAGTTAACGACC AGCCAGGGCACCTAGTGGACTT CTATATCT	Induced in Individual 7, but not in Individual 6	AC004531

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
141	C + AP41	No significant match to anything	464bp	CAGGGGAGGGGACACCACTCAA ACTATTTAAACCTTACAGCAACGT GACCGTGGATAAATTATACAATTAT AAGTGTGAGGATTCTTAATAAAAA ATATAAGGATTGAAATTAAATATT CAAACATCAAGAAAATAGACACATA TGTAACAATAATCCAGACTAAAGAA ATGTCAGCATTTGTCAATTATTA CATTTTTAACCTTTAAAAAAATGA GATATTATAGATAAAAACAACCTCTCC ATCTCATTCTCCTCCTACCTCTCC AAATAATAGTCACACTTCCTGAAGTA TGTTTGCATTCAATAGCAATTTTATTAA TTTTAGTATTGCATACTTGATGATG CAAGTAAACTAACTTAACTTTAAACT GCTACATCAGAGACCTTGAATTGA AATTGACTTCTGAGGCCTCAGAAT CTTTCATAATAATTCTGCCCTAGCC ACCCCGTAAGGCT	Induced in Individual 1 and Individual 7, but not in Individual 6	M90727
142	C + AP41	Fc-gamma-receptor IA (FcGR2A)	240bp	AAGCTTACGGGGTCACTACATA CAAGCATAAGCAAGACCTAACCTG GATCATTCTGTAAATGCTTATGT TAGAAATAAGACAACCCAGCCAA TCACAAAGCAGCCTACTAACATATAA TTAGGTGACTAGGGACTTCTAAGA AGATACCTACCCCCAAAAAAACATT ATGTAATTGAAAACCAACCGATTGC CTTATTTGCTCCACATTTC ATAAAATACTTGCCCTGTG	Induced by penicillin in Individual 1, but not in Individual 6	
143	C + AP45	Chromosome X clone bWxD501	67bp	CGATAATAAGAACCAAAAGAAATT ATTACAAAATTCTTACTTGACCAG TAGGTCTAGCCCAAGCTT	Induced in Individual 7, but not in Individual 6	AC004677

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
143	C + AP45	clone CTA-407F11 on chromosome 22q12	64bp	AAGCTTGGCTGACAATCTCAGAGG TCACCTTTATAGAAAAATATAGTCT AGGCTTAGGTTCCCTG	Induced in Individual 7, but not in Individual 6	AL022329
144	C + AP48	3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene	104bp	CAAAACAGTATTATTATTTACAAAT AGCAACCAAACTCCCCAGTTTGTTC AATTGTGACATCTAGATGGCTTAAAG ATTACTTCTGGTGTCTACCGCAA GCCT	Repressed in Individual 1, but not in Individual 6	U80460
145	G + AP53	SH3-containing protein EEN (EEN)	253bp	GTAGAAAGAGACATTAAATACCTCT GTTTACAAAATTCAAGGGGTACATT CAGTTTGCCTGNACCGTGCCCAA AGCTGTGTGCTCATCTCTGGGCC CTCATGTACTTCTGACGAGGGGG TGCAGGGCAGGGCAGAGCAAGGC CTGGGGTCCGGAGGGCTCACGTGGA CCACAGGGGAGGGGAATGTGAAT GTGGCCCTGCCAGAGAACTCCCCA TTTCATCGATTTCGATTGGGGAT AGAGGAAGCTT	Induced in Individual 6, but not in Individual 1 or Individual 7	AF190465
146	G + AP53	SH3-containing protein EEN (EEN)	255bp	GTAGAAAGAGACATTAAATACCTCT GTTTACAAAATTCAAGGGGTACATT TCAGTTTGCCTGTGACCGTGCCATT AAGCTGTGTGCTCATCTCTGGGCC CCTCATGTACTTCTGACGAGGGGG GTGCAGGGCAGGGCAGAGCAAGAG CTGGGGTCCGGAGGGCTCACGTG GACCACAGAGGGGGAGGGAAATGTG AATGTGGGCCTGCCAGAGAACTC CCCATTTCATCGATTGGCATGGG CGATAGAGGAAGCTT	Induced in Individual 6, but not in Individual 1 or Individual 7.	AF190465
147						
148						

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
149	G + AP55	No significant match to anything	287bp	GTAATTGGTTGAGTCATTGTAG ATTCTGGATATTAGCCCCTTGTCA ATGAGTAGGTTGTAAAATTTC CCATTGGTAGGTTGCCCTGTTCTC CTGATGGTAGTTCTTGGCTGTGC AGAAGATCTTAGTTAATTAGATC TCATTGGCAATTGGTCCTTTATTG CGGTTGCCCTGGCCATGCCCTATGGC GAAGTCCTGGCAATGGCTATGGC CTGAATGTAATGCTTAGTTTCT TCTAGGGTTTATGTTTATGTC TAACGTAAGCTT	Induced in Individual 1, but not in Individual 6	
150	G + AP54	ribosomal DNA complete repeating unit	215bp	AAGCTTTGAGGTCAAGGAGTCGA GACCAGCGTGGCCAAACGTTGAGA AACCCCGTCTACTGAAATAGG AAATGAGCCGGCGTCATGGTG GGCCTGTAATCCCAAGCTACCGAA GAAGAAATCACTGGAAACCGGGAA CAGAGGTTTCAGTGAGCCGAGAGA GCGCCACCGCACGGCAGCTGG TGACAGAGCGAGAGACTGTC C	Induced in Individual 1, but not in Individual 6	U133369
151	A + AP52	heat shock 60kD protein 1 (chaperonin) (HSPD1)	241bp	AAGCTTGACCTTTATAATGAACTG TGACAGGAAGGCCAAGGCAGTGT CCTCACCAATAACTTCAGAGAAGT AGTTGGAGAAAATGAAAGAAAAAGG CTGGCTGAAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAT ATATAATGGTTACTGCTGTCAATT TCCATGCTACAGATAATTATT GTGTTTGAATAAAAACATTGT ACATTCCCTGATACTGGGT	Induced in Individual 6, but not in Individual 1 or Individual 7	NM_002156

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
152	A + AP52	cDNA FLJ20436 1s, cDNA KAT03972	204bp	AGGGGAGGTGCTAGTAGAGGA ATCCCTTATGATCAACTAGAGCT GGTCCTCACITCAGTCGAGTG CTGTCCTCATTAGACACAGTAAGAG AGTTAACAGGTACCCAATGGCAGT CGCATCTTCTGGTAAGGCAGTG TCTGGTCATTGGAAAGGAGCTGATT GGAACAAACGAAACATCATCCACAAA GGTCAAGCTT	Induced in Individual 6, but not in Individual 1 or Individual 7	AK000443
153	C + AP55	No significant match to anything	407bp	AAGCTTACAGTTAGAACCTGCAATAT TCTCGTGTGTTGTTGCTTCTCTT CCTGTCACAGTGTGTTATGCTTCC CAGCAGCAGACACGTATGTTGTA CACACATACTCATTCAATTTCATT TTAGGAAAGGCCATTACACATGA AAAACAATTGAGATAATGGTAGTG TTTTTATGGGTATTCTAGCACCCA TAAAGCAATTAGGAATTAACCATT CCCTTTCTTAATAGGATAACCAGCT TGAGAGAAGTGTGGTCATATTCT ACAGCCTCATAATAGTAAAGTCAGT GTCTTCATCACATGGACTCAGCATA CTCTTAGAACTCCTTTAGTGGGT CAAATCTAGATNTACTTGCCTCCAT TTTATTATGG	Repressed in Individual 1 and Individual 7, but not in Individual 6	
154	A + AP47	Sid3177 mRNA (This is a mouse gene)	95bp	AAGCTTATGCCGGCTGAAAAAC TCAATTATGTTCATGACAGTGGGG ATTTTTTAATGTCTACATTCTTC TAATAAAACTGTTGGAAGACT	Induced in Individual 8 and Individual 10, but not in Individual 9	AB024935

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
155	A + AP47	Chromosome 16 BAC clone CIT887SKA-67A1	106bp	AAGCTTATGCCGTAATTACCGCAT TTTGGAAAGGCCAAGCAGGAGAT CACTTGAACCAAGAGTTAACGACC AGCCAGGGCAACCTAGTGGACCT CTATATCT	Induced in Individual 10, but not in Individual 9	AC004531
156						
157	G + AP41	ribosomal protein L8	218bp	GGCATAAACACAACCTTATTGAGG CCCTCAGCACTAGTTCTCTTCTCC TGTACAGTCTGGTTCCCGGAGA CGTCCAGTCCGGGGCAGCAAT GAGACCCACTTGGCCAGCAG GGCATCTCGGGATGGTGGAGG GCTTGCCGATGTGCTGGTTGC CACCTCCAAAAGGATGCTCCACAG GATTCAATGCCACACCCCCGTAAGC TT	Induced in Individual 10, but not in Individual 9	NM_000973
158	G + AP41	tapasin (NGS-17)	58bp	GGAAGGCACTGGAATACAGCTTTATT CCTACACGATTAGACCCGTACCC CGTAAGCTT	Induced in Individual 10, but not in Individual 9	AF029750
159	G + AP47	CoREST protein (CoREST) (KIAA0071 protein)	149bp	AAGCTTATGCCGAAACAAAAAC GGGAGGGGGAGGGAGGCGGAGGAT GAACCTGGAAAGGGCAAATGGAAAC ATCCCATGGACATTGGAGGTTGATC AAAACAAGGAAAGCAAAAGGGG TTCCCCCTACTGAGACAGTTCCTC AGGTC	Induced in Individual 10, but not in Individual 9	AF155595
160	G + AP43	mitochondrial DNA hypervariable II region	104bp	GTAGGACATAATAACAAATTGAA TGTCTGCACAGCCGCTTCCACAC AGACATCATAACAAAAATTCCAC CAAACCCCCCTCCGCTTC AAGCTT	Induced in Individual 10, but not in Individual 9	AF278478

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
161	G + AP52	clone RP11-517O1 on chromosome X / FLJ23025 fis, clone LNG01702	71bp	GGAGACAAATAACAGTGGCATTAC TGGAGGAATATCACACATTACAT TTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
165		clone RP11-517O1 on chromosome X / FLJ23025 fis, clone LNG01702	71bp	GGAGACAAATAACAGTGGCATTAC TGGAGGAATATCACACATTACAT TTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
162	G + AP52	clone RP11-517O1 on chromosome X / FLJ23025 fis, clone LNG01702	71bp	GGAGACAAATAACAGTGGCATTAC TGGAGGAATATCACACATTACAT TTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
167		clone RP11-517O1 on chromosome X / FLJ23025 fis, clone LNG01702	71bp	GGAGACAAATAACAGTGGCATTAC TGGAGGAATATCACACATTACAT TTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
163	G + AP52	clone RP11-517O1 on chromosome X / FLJ23025 fis, clone LNG01702	71bp	GGAGACAAATAACAGTGGCATTAC TGGAGGAATATCACACATTACAT TTTATCTTAAGGTCAAGCTT	Induced in Individual 10, but not in Individual 9	AL355476
169		No significant match to anything	103bp	CAAATTGTATTCCTTTATGAAATT AATATTCTCAACTAGTATCAATGCT TTGTCAATTAAAGTGTGACTTCA ATATTTCCCTCCCTCACCGCAAG CTT	Repressed in Individual 8, but not in Individual 9	
164	C + AP48	dynamin (dynactin complex 50 kD subunit) (DCTN-50)	61bp	CAGAGTACAACAGCATTAAATGGTC AGAACACGTTACAGTATTACAGT CAGCCCAAGCTT	Induced in Individual 10, but not in Individual 9	NM_006400
165	C + AP45					

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
166	A + AP3	cyclin D2 (CCND2)	265bp	<pre> AGGTCAAGGTGAGTTTATTGTC ATAGCATAACCTAATGCAATTCAA ACCATTCCAATCCATCCTTAAAC TAGTCAGAAAACAGGTTATTATTT TTAAATCACCTAAACACTGAACAGA TAAGACCTCTTAAAGGCCAGCTGA CTATATCATGTCAACATCATGCCA ATACAACATTGGCATACTCTCT AAAAACCTTTTGCAATACACTGATC ATGCTACTTATCAACACTTCTAAC ATCCTGACCAAAAGCTT </pre>	Induced in Individual 11, but not in Individual 12	NM_001759
167	C + AP24	chromosome 16 clone RP11-296110	246bp	<pre> CCATACATAGGCTTGAACAGGGTT CAGCCAACTCTCTGCAGAGGC CAGAAAGTAACAGTCTCAGGGAA CTGTAGTCACIGTGTGAGTTACTCA ACTTGGCAATCCTAGTGTGAAAAGC AGCCCACTGGCAATACATAAAATAAT GGTGTGGCTGTTCAATAAAATT ATGTATAAAACAGGGTAGTAGCTG GATTGGCCTAAGTGTGTAGTTT TTGATCTATGGCTAGTGAAGCTT </pre>	Induced in Individual 5, but not in Individual 12	AC0009060
168	C + AP24	No significant match to anything	253bp		Repressed in Individual 11, but not in Individual 12	

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
168	C + AP24	NADH dehydrogenase	254bp	CATTTTATTTTATTAAAGCACTACAT AACACATTGCATGCTACATAATTACA CTGTAACCTCTAGCAGGGTAGA TGGCCATAACTGAGTTATT-TTTC ATCAATCAGGAAAATGCTTCCCTAA TCAATGTTCTCCAACCCCTTGACAA CATAGTAACCGATCAACTCCAGAGAT GCGCCTATCTCTTCCATCAGACTC CAGTGATACCCAAAATGAGCAACC CTTTTCCCTGCCCGCTAGTGA AGCTT	Repressed in Individual 11, but not in Individual 12	X81900
169	G + AP5	alpha-L-fucosidase	153bp	AAGCTTAGTAGGCTGCTATGGTCA ACTCTCCAGAAATTTCAGAGCAAT CTAAAAGGCCAAAATTGCTATGT TTACAGTGATACTATTAGAAAATG AAATGTGATTCTGCTCTGTCTTTTA AGTATGATCAAATAAAAAATTGTA CATC	Repressed in Individual 5, but not in Individual 12	M29877
169	G + AP5	latexin mRNA	139bp	AAGCTTAGTAGGCCAAATAATCCCA AAGGTGTCACTTTATATAATGTCTT GATTACAGTATAAGAACTTTATAGAG TCCATAATAACAAAGTATCACTACAT AAAAATGTCTTAAACAGTAATAG TGGTATGTATATCC	Repressed in Individual 5, but not in Individual 12	AF282626

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
170	G + AP10	manganese superoxide dismutase (MnSOD/SOD2)	294bp	AAGCTCCACGTATAAACATAAAATTGTTTCCCTGTTTAATTCAGGGGAGTACTGTGTTGGAAAGCTTATTAGGTAATGTTTACAATTACTGTTCTCACTTCAGTCATAACCTAATGTCCTGTTCTAAGATGTGCATCAAGCCTGTTACATACTGAAAACCTATAAGCTCTGGATAATTGGTTGATTATCATTTGAAGAACATTATTTCCAATTGGTGAGTTTGACTGTAAATTAAAAGAAATGTCAACCATCGGGAAATCAAGTCTAAGTGTTTAATTATTTCACATTTCACAGAAAAAGGAATGTAGCAAAGGGGTCAAGATTGTAGCAAAAAAAATCCTGGATTTTACGGGTCACTCTATTATACGTGGAAAGCT	Repressed in Individual 11 and Individual 5, but not in Individual 12	X65965
171	G + AP10	metallothionein-1G (MT1G)	137bp	GGGTCAAGGTGAGTTTATTGTCCAAATAGCATAACCTAATTGCAATTCAACATTTCAAATCCATCTTAAACAGTCAAGAACAGGTATTATTTTAAATCAGTAAACACTGAACAGAAGCTT	Induced in Individual 11, but not in Individual 12	J03910
172	A + AP23	cyclin D2 (CCND2)	179bp	ATAGTCAGAAACAGGTATTATTTTAAATCAGTAAACACTGAACAGAAGCTT	Induced in Individual 11, but not in Individual 12	NM_001759

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
173	A + AP3	cyclin D2	265bp	AGGTCAAGGGTGGAGTTATTGTC ATAGCATAACCTAATTGCATTCAA ACCATTTCATAATCCATCTTTAAC TAGTCAGAAAACAGGTTATT TTTAATTCACCTAACACTGAACAGA TAAGACCTCTAAAAGGCAGCTGA CTATATCATGTCACCGATAGGCC ATACAACATTGGCATACTTCC AAAAAACCTTTTCGCATACACTGATC ATGCTACTTATCAGCACCTCTAAC ATCCTGACCAAGCTT ACATTCTTCAAAAGGGTCTTTATA GAECTGTCCATGTCTTCAATCAA TATCTCTAAATTGTATATTACTACCT TGCGCTCTAAATTAGTTTCCCTCC TAACAAGCAAGGAAATGGAACAGG TAATATCTAAAATTAAGTAAACCC ATGGAATAGTTCTAGGACTCTGAC CAAAGCTT	Induced in Individual 10, repressed in Individual 9	NM_001759
174	A + AP3	clone RP11-120K22 on chromosome 6	182bp	GGAAAAACATCACAGAATAACTG TTCCAGATTCTTATTGTTCTCCAAAC CTTCAAAAGAAACTCTGGAGTTATT TCCAAGGGAGGAAGTTGACCTGC ATTGTGTCCCCAGGACCTGCGTAA TCACCTTCCATGCACTGTCACTCAT CTTCTATGAGTTCTAGCTTGTCCAA TGCAACAAACAGGCCACAACTCTCA TCACACTGAAAAGCTGTTTCCCTT GGTAGACCCCCGTAAGCTT	Induced in Individual 1, but not in Individual 9	AL137178
175	G + AP41	Familial Cylindromatosis cylid gene	241bp		Repressed in Individual 11, but not in Individual 12	AJ250014

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
176	G + AP41	ribosomal protein L8 (RPL8)	218bp	GGCATAAACAAACTTATTGAGGCCCTCAGCACTAGTTCTCTTCTCC TGACAGTCCTGGTTCCCAGGAATCGTCCAGTCCGGGGCAGCAAT GAGACCCACCTTGCAGGGCAGCAGGG GGCATCTCGGGATGGTGGAGGC GCTTGCAGTGCTGGTTGC CACCTCCAAGGATGCTCCACAG GATTCAATGCCACACCCCCGTAAGCTT	Induced in Individual 11, but not in Individual 12	NM_000973
177	G + AP42	No significant match to anything	241bp	GATACTAAATGGTTTGCAGAA AAAGGGATGAAACCTACTCTTAAAC CACCCGAGTAACCAAGCTGCTACT AAGACTAGAGGGATGCTAATTCTG GCAAAAGTCAAAGGTACTAACAAA AATTAGCTAAGATTATGTTGCA GAAAGTCAATTAGGGTAATTCCG CTATTATCCTGGTGTATTATTCC CTAAATAACTGGCAATTCCACCTTAA ACTACGGTGCAGGCTT	Repressed in Individual 11, but not in Individual 12	

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
178	G + AP42	cDNA FLJ10589 fs, clone NT2RP2004389	330bp	GAAACTAACATTCTTTATTTCC TATTTTTAAAGGTCAACCTTACAAA GTAGCATTAAAAATAAAATCCATCT CACAGCTCAAAGAAATTCTGACAG TACTGGCACATATATAAGCTCTCT TCGCCCTTCATGCTGGTCAGCCA TTATTTACTGTGTGTGCCACATG ACGGTTTCTCCACGTAACCTTCT GGGGGCTCCCTCTGGCCTGGCTT CTTCCGTTCCCTCACACGTGGATC AGTAGTAAGTAGTGTCAAGCTGTCTC ATCCACTCGACCTCGCTCGGGTG CAAAGCTT	Repressed in Individual 11, but not in Individual 12	AK001451
179	G + AP47	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D)	217bp	GCCGGTCTCAGTCTTTAATCGGG CAGGGCCTCAGGCAGGGGAC GTACACACACTCAGGCTCAGATC TTGTTGAAAGCTGCAGATCGACA CTCTGCACGTGCTCCAACTTG GTGATCTCCTCCAGCAAGTCT GTCCCCACCTGGTCGTCCACC ACACACTGAATCTGTAGCTCCGG ATACCGTAGGCCACGGCATTAAGC TT	Repressed in Individual 11, but not in Individual 12	NM_001960

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
180	G + AP47	Chromosome 16 BAC clone C1T987SK-A-67A1	270bp	GATTCAGGGTCICGTTATGTCACCT AAGCTCACAGTGCAATGGCACAATC ATAGCTCAACACAACAAACCCCTGAGTTTC TGGGCTCAAAGGATGCCCTCCACTT CAGSTCTCTAGTAGCTAGCTAGGACAT CAGGAGTGTGCCAACAAACCTAGC TTTTTTTTTTTTTTTTTANATAAGA AGTCCCACACTAGGTTGCCCTGGCTG GNCTTAACACTCTGGTTCAAGTGA TCCTCCCGCCTGGCTTCCAAAT GCTGGTATTACGGGCATAAGCTT	Induced in Individual 5, but not in Individual 12	AC004531
181		No insert - just vector				
182		No insert - just vector				
183	A + AP41	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7) (PSMB8)	451bp	AGCTTACGGGGTCAATGGACAGTGG CTATGGGCCCTAATCTTAGCCCTGAA GAGGCCCTATGACCTTGGCCGAG GCTATTGCTTATGCCACTCACAGA GACAGCTATTCTGGAGGGCTTGTCT AAATGTACACATGAAGGAAGAT GGTTGGGTGAAAGTAGAAAGTACA GATGTCAGTGACCTGCTGCACAG TACCGGGAAAGCCAATCAATATGG TGGTGGGGAGCTGGCAGTGGCAGGTC TCCTCTGGGGAGGTCTTGGCCGACT CAGGGACTTAAGCCACGTTAAGTC CAAGGGAGAAGAGGGCCTAGGCC GAGGCCAAAGAGAGGTACGGGCTC AGCAGCCAGGGGGGGGGTGA GTGCATCTTCGCTGTTCTCTATT TGAAACAAGCATTTCCCCAGGGAA GTTTCTGGGTGCCCACTAAGTAG AATAAAGAAAAACGGTTAT	Expression is higher in individual 5 and individual 11 then in individual 12	NM_004159

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
184	G + AP42	lectin, galactoside-binding, soluble, 9 (galectin 9)	153bp	AAGCTTTGCACCGTGACCAAACCC TTQACCCCTCCTGGAAAGCAGGCC TGATGGCTTCCACTGGCCTCCAC CACCTGACCAGAGGTCTCTCTCA GAGGACTGGCTCCCTCCAGTGT CCTTAAATAAAGAAATGAAAATGC TTGTTGGC	Repressed in Individual 5 and Individual 11, but not in Individual 12	NM_002308
184	G + AP42	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	201bp	GACTATCTACAAAAATTATTATA TTTACAGAAAGAAAAAGCATGCATTC ATTAAACAATAAAATACTTTTATC ACAACACAGTACATATTGTCAATT TTAAAAAAGCCACACAAATAGAAAACAA GACACCAAGATAATTAAATTATCTG TTGACTCCTGTAAAATAGCTAAACA CTCATCATCGGGTGGCAAAGCTT	Repressed in Individual 5 and Individual 11, but not in Individual 12	NM_000938
185	A + AP47	Chromosome 16 BAC clone C17897SK-A-67A1	106bp	AGATATAAGAGTCCCACTAGGTG CCCTGGCTGGCTCTAAACTCTTGG TTTCAGTGATCCTCTGCCTTGG CCTTCCAAATGCTGGTATTACGG GCATAAGCTT	Induced in Individual 11, but not in Individual 12	AC004531
186	A + AP46	UbA52 gene coding for ubiquitin-52 amino acid fusion protein	103bp	ACACGACTGAGGTTTACTCCAGT TTTACAGATGACAATCCAGAGTCA GGGCATAGGGCAGGGACCAATG CCGATGTGACAGAAATCTAGGACCG AAGCTT	Slightly induced in Individual 11, but not in Individual 12	X56997

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
187	A + AP44	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) (SNRP70)	206bp	AAGCTTCTCGGAGAATGGGTATT TGATGGAGGCTGCCGGAGATGA AGAGGTCGTCCTCTCCATCTGCTG TGTTGGACGCGTTCTGCCTGCCAGC CCTTGCTGTCAATCCCCCTCCCCA ACCTGGCACITGAGTTGTCTCATTTGTT CCAAGGGTAGGTAGTTAAATAAA ATTAAATTCTCTGTT	Induced in Individual 11, but not in Individual 12	NM_003089
187	A + AP44	Isocitrate dehydrogenase 3 (NAD+) gamma (IDH3G)	204bp	AAGCTTCTCGGACATCGGGGCC AGGGCACAAACATCTGAAGGCCATCC AGGACGTCATCCGCCACATCCCG TCATCAACGGGGGGGGGGCTGGAG GCCTAGGGCTGGCCCTAGGACCTC TTGGTTTGCTCTGGATTCCCTT CCCACTCCAGCACCCAGGCC TGGTACGCGAGATCCAGAATAAG CACCTTCTCCCT	Induced in Individual 11, but not in Individual 12	NM_004135
188	A + AP44	no insert - just vector				
189		clone RP4-646P11 on chromosome 1	238bp	AAGCTTTGAGACTAGCCTGGGCAA CATGGAGAAACCCATCTCCACTA AAAATACAAAAAGTGGATGGCAT CTTGGGGGGCAACTGTAATCACCA CTAATGGGAGGGCTGAGGCAGAAG ATCCCTTGAACCCAGCAGGAG Repressed in Individual 11, but not in Individual 13		AL049715

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
190	A + AP52	hypothetical protein FLJ20436 (FLJ20436)	204bp	AGGGAGGTGTGCTAGTACAGAGGA ATCCCTTTATGATCAACTAGAGCT GGGTCCCTTCACTTCAGTCGAGTG CTGTCCTCATTAGACCACAGTAAG AGTTAACAGGTCAACCAATGGCAGT CGCATCTTCTGGTAAGGCAGTG TCTGGTCATGGAAAGAAGCTGATT GGAACAACGAACATCATCCACAAA GGTCAAGCTT	Induced in Individual 11, but not in Individual 13 or Individual 5	NM_017822
191	G + AP49	c-Cbl-interacting protein (CIN85)	317bp	AAGCTTAGTCATAGGGTACTAT TTTGATGATAATTTCCATTAATAAAA TGTAATTTCAGATTTCGTTTACAA GCTTTATAAATTTATGATTTTTAAT CGTGTGTTGTCACAGACCTCCCTAG TGTTTGTACTACACGTAGTCAGAAG CGAGTGTCTTTCTTTGCTTCAG GCTAAGAGGCTGCCTGCTCTTGT CCCCCATTATGATTCTATTACATA TGCAATTGTAAGGTTCAACCTGTCCC TTTCCCTGCCAGCAAACCCACCA CCCTAAGAGAAATTAGCTTAT ATGACGGTATATTAC	Repressed in Individual 11 and Individual 5, but not in Individual 13	AF230904

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
192	G + AP49	ribosomal protein L7a (RPL7A)	293bp	GGCTGAAGGAAATTGTATTATT CAATTATTTATGTACAGAAA CAACAGTGACATTACCCAGTT AGTGGCAAGTTCTTAGCCTTTGCC TTTCGAGCTGGCAATACGAGCC ACAGACTTAGGACCCAGGACATG CACACCCAGTGACGGGGATCTCA TCGTATCTGTCAATTGTAAATTGGTCC TGATAGCTTCCACCAGCTTAGCCA AAGCGCCTTGTCTTCCGAGTTCA CCTGTGTGAAGGGCGACAGTGGTGC AGGTCTTCTGTGGACTAAAGCTT	Induced in Individual 11, but not in Individual 13	NM_000972
193	G + AP51	ribosomal protein S21 (RPS21)	318bp	GTTAGGTTTCATTATTTATGA CAAATATTCCACATCTGTGATTCTC TCCAGTCAAAAGTTCTTGAGACGA TGCCATCGGCCCTGGCCAATCGGA GAATGGAAATCATCTGACTCACCCT CCTACGAAATGGCCCCCGCAGATAGC ATAAGTTAAACTGGCCATTAAC CTGGCTGTGACCTTGTCAACCTCG GCCACGTTCATCTGGATGGATGCG TGGCTTAGGGAGCATTTCCGGGC ACGTACAGTCCACGAACTGC GGCTCGTTCTGCATTTCGAAGCTT	Induced in Individual 11, but not in Individual 13	NM_001024

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
194	G + AP50	Chromosome 16 BAC clone C1T887SK-A-87A1	150bp	AAGCTTTGAGACTTGGAAAGGTAC GCTGCTGCCAGCATTGGAGAAGA AGCTGCTGAGCATGGCTTTCTGTA GTCTTTAGCAAGACACAAGTGATT TTGACTTTGTATCATGTCATGATT CTAACAAATAATGATGTTTATGT GCC	Induced in Individual 11, but not in Individual 13	AC004531
195	G + AP50	sorting nexin 6 (SNX6)	132bp	AAGCTTTGAGACTAAACCAAGTATT GTAAAAATAAACAGCGATAAACAGTGA TAGTTTTTAACTCTATGGTCATTGT ATCACTCTGGAAAATGTGGAGTAG CTGTAATAATCTACTCCCTGTATTAA TGCTTAC	Repressed in Individual 11, but not in Individual 13	AF121856
195	G + AP50	No significant match to anything	133bp	AAGCTTTGAGACTATGTACAATAAC ACTAAAGTGGTGTATGGTGTACAATA TTGTNAAGAATTATTCTGTATAAAAT GAGAAACTGGATAATAATGTCAAAAAT AAGCTTATTCTCAATAAAAATCTC AAATCTCC	Repressed in Individual 11, but not in Individual 13	
196	G + AP50	TNF-inducible protein CG12-1 (CG12-1)	87bp	GGTGAGTAGGTGAGTTATTAGGA CTTACACACAGGGCACTCAGCAGG ATGGCTCTAGAGATCGGCCTCCC CCAGTCCTCAAAGCTT	Repressed in Individual 11, but not in Individual 13	NM_014349
197	G + AP50	BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA	55bp	GTATTTAGTAGAGATGGGGTTTC ATCATGTCGCCAGGGCTAGTCTCA AAGCTT	Repressed in Individual 11, but not in Individual 13	Z75887 Z75888
198	G + AP51	ribosomal protein S24 (RPS24a)	160bp	GAAGTTTTAGTTTATTAATGTTCTT GCGAAAAATCCACAGTGGCCACAG CTAACATCATTTGCAGCACCTTACT CCTCGGGCTTTGCAGCCCCCTGA CTTTCTTCATTCTGTTCCTGGCTTC ATTTCGAAGCTT	Repressed in Individual 5 and Individual 11, but not in Individual 13	NM_001026

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
199	G + AP51	No significant match to anything	120bp	GGCATCTGGGTTACTATACTCACT CATGCCAAATCCAAGGTAGTGTAAAT GGAAACAATATTGGTAAAATAGATG TTGGCTATAAGCATCCTCTTA TATTAGACATTTCGAAGCTT	Repressed in Individual 11, but not in Individual 13	
200	G + AP52	CGI-128 protein mRNA	146bp	GGAAACTGAATAAATTAACTTTA TTACAAAAAGCAAAATGTTAGTTTC TCATTGTGAGTGATTCAAGAAAACA ACGGTAACAGCCCTGGCAGGAGCT GGGACCAAGGATAACCAAGTATGCAG CTGGGGTCAAAGGTCAAGCTT	Induced in Individual 11, but not in Individual 13	AF151886
201	G + AP41	ribosomal protein L8 (RPL8)	218bp	AAGCTTACGGGGTGTGCCATGAA TCCCTGGGAGCATCCTTTGGGG TGCAACCACCCAGCACATGGCAA GCCCTCCACCATCCGGAGAGATGC CCCTGCTGGCCCGCCGGACTGGACG CATTGCTGCCGGAAACCAAGACTGTGCA TCTCGGGGAAACCAAGACTGTGCA GGAGAAAGGAACCTAGTGTGAGG GCCTCAATAAAGTTGTGTTATGC C	Induced in Individual 11, but not in Individual 13	NM_000973
202	G + AP41	Familial Cylindromatosis cylid gene	241bp	GGAAAAACATCACAGAAATAACTG TTCCAGATTCTATTGTTCTCCAAC CTTCAAAAGAAACTCTGGAGTTTAT TCCAAAGGAGGAAGTTGACCTGC ATTGTGTCCCAGGACCTGGGTAA TCACCTTTCGAATGCAGTGTCACTCAT CTCTATGAGTTCTAGCTTGCCAA TGCAACAAACAGGCCACAACTTCA TCACACTGAAAAAGCTGTTTCCCTT GGTACACCCCGTAAGCTT	Repressed in Individual 11, but not in Individual 13	AJ250014

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
203	G + AP47	Tu translation elongation factor, mitochondrial (TUFM)	358bp	GGCTTACTATTCAAAGTTACTGAC CTCCCCAAGCCAGGAGGCCAAC CTTCGAGCGGGAAATGTCCAT CTAGCTGCCCTCTGCTGGTTGCA GCCTATGCCATGAGGGGTACTGG AAGCAGGGAGGGAGGCCCTGGCTAG GGCAGGGCTTAAACGCAAGGAAG CTGAGGAGAGATCTGCACACTCAA CCCCATTGATAATTCTCTCCT CAGTCATGGCCAGCGTGTGGCTGA CTAGACCGGTGCCAATAGTCGGGT TGCCATCTCGCAGGGTGAACAGCT GGCCTTTCTCTAAGATCATGGGCTG CGGCAAGATTAGGTTGAACCTCAN GTCCTCCCGGGCATAAGCTT	Induced in Individual 11, but not in Individual 13	NM_003321
204	G + AP47	KIAA0787 protein	200bp	AAGCTTATGCCGATGCTCTGTTT CATTCGGACCCCTTCTACTATGCA TTTCCCTTTATCAGGTGATAAAG TTAAATACTGTGTATTATCACTAAA AAGTACATGAACCTTAAGAGACAAC AAGCCTTCTCGTGTTCACAGGT GTTAAAGCTTCTGTACAGTTGAA ATAAACAGACAGCAAATGGTGCC	Induced in Individual 11, but not in Individual 13	AB018330
204	G + AP47	ribosomal protein L13 (RPL13)	203bp	GATTCCAAGTCCCAGGGCCTT TATTTTCCTTCAACATCCTGTT TGGGCTTCTCTGGCTCTTTGCG CGGTATGCCGAAGAGCGGGCGTT GGCACGGGCCATACGGAGACTAG CGAAGGCCTTGAATACTCTCTC CTCAGTGTACTGAGCTTCTCTC CTCTTATAGACGTTGGGACGGG CATAGGCTT	Induced in Individual 11, but not in Individual 13	NM_000987

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
204	G + AP47	fatty acid synthase/ NY-REN-57 antigen RNA	202bp	GGAGATCACATGCCGFTTAATTGTGGGGCTGTAGAGCGACGCATTTACAAATTGGTGTAAAATGAAACGCCAAGTCAGTAAATTCAAAATCCAAAGCTTACAGATTGAATCATTTCTTGAAAAACAAACACAGACAAACACCAAACATGGAGTTGGTGCCCGGCCGGC	Induced in Individual 11, but not in Individual 13	S80437
218				AAGCTTATGCCGCAAGGTCTAAGACCAAGGAAGGCACGCCAAGGCCGTGAAGAGGCCCTCCAGGCCAAGAA	Induced in Individual 11, but not in Individual 13	NM_0000881
204	G + AP47	ribosomal protein L19 (RPL19)	198bp	GGAGGAGATCATCAAGAACCTTATCACAAGGAAAGAGAACCAAGAAATAAACACCTCCACCTTGTCTGTACATACCTGGGCCTCTGTGATTACATAGATCACGCCATTAAAATAAAACAGCCTTAACTCTGC	Induced in Individual 11, but not in Individual 13	
205	G + AP45	clone 245M18 on chromosome 6p21.32-22.3	186bp	GAAAGGAATATTCTAAATGATAAGATATGCTCTGGCTACACAGCACAAATAAAGATGGTTTAGCTTACATGATCTGATTGTCTGTCAACAGAATCCAACAGTTCAGGCTTGTGACACGTCCTCTTCAGCCTAGGGTGTGCA GATGTTATGGAATCATCACCCCTCATAGTCAGGCCAAGCTT	Repressed in Individual 11, but not in Individual 13	AL078584

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
205	G + AP45	clone TCBA00781	184bp	GAATGTCCAAATTGTTTATTAGT ATGAAATTACAAACTTACTTATAT TAGGGTAACGGGGAGCTGGAGA GTATTGCGCTTCTCAAGCTGCC CGGCAGAGGCCACCAATAGTGTGG TGGAACTTGTGGCCCCCTCCAAGG CACGGCTCTTGGCTGCAGAT GTCAGCCAAGCTT	Repressed in Individual 11, but not in Individual 13	AF283772
206	G + AP45	chromosome 19, cosmid R26529	198bp	AAGCTGGCTGACGTTATGGTGGC TTCAAGCTTCACTAGGAATGGGACA CAAGGTCTGGGGCTCTGACTCC CCCACCCCCGAGGGCTGGTAGGG ACAGGGGTGGTGTCCCTGGTGG GTCAGGTAGGGCACAGGGCCAG GGAGGGACAAAGCAGACCTCAGAG CGCTGCCCAAGATGGAAATTAATT ATTTTGGCC	Induced in Individual 11, but not in Individual 13	AC005551
207	G + AP47	tumor suppressing subtransferable candidate 1 (TSSC1)	182bp	CGAGCGTGATTATTATTCAT TTTTTACTCTCAAGAGAAAGAGAG TTAAGCTGAGAACAGACATT TTAAAAAGCGAAAACTCCCTGACACC CTAAAAACAGAAAAACATTGGTTATC ACATAATAATGTGGGCTCTGTCCT TGCCGACAGGGCTGGGGTCCGG CATAAGCTT	Induced in Individual 11, but not in Individual 13	NM_003310
208	G + AP43	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	74bp	GTTGAGCACAGGGTACTTATTG ATGGTACATGACAAGGTGGGCTC CCTAGGGCCCTCCCCCTCAAGCTT	Induced in Individual 11, but not in Individual 13	AF261085
209		no insert - just vector				

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
210	G + AP52	transferrin receptor (TFR)	105bp	GCACATAACAGCTTTATACAATGATAAGGACATATCATTGTTACAAACAAAGCTAACACAGTAAGGTCAGCTT	Induced in Individual 11, but not in Individual 13	AF187320
211	G + AP55	Homo sapiens PAC clone RP4-649M7 from Xq23	287bp	GTAAAATTGGTTGAGTTCAATTGTAGCCCTTGTCAATTCTGGATATTAGCCCTTGTCAATTGAGTAGGTTGAGTTGAAATTTCCTCCATTGGTAGTTGCCTGTTCACTCTGATGGTAGTTCTTGTGTTAGTCAGAAGATCTTTAGTTAATTAGATCAGAATTCATTGGTCATTGGTTGCTTTATTGCGGTGCCCTGGCCATGCCTATGGCCTGAATGGTAATGGCTTAGGTTTCTCTAGGGTTTATGGTTTATGTC TAACGTAAGCTT	Induced in Individual 11 and Individual 5, but not in Individual 13	AC006968
212	G + AP54	ubiquitin-conjugating enzyme E2D 3 (UBE2D3)	142bp	AAGCTTTGAGGTACATGATATGCTTATGGCTCATAACTGATGGCTGGCTGAGAATTGGTATTGAAATTATAGCATCAGCAGAACAGAAAATGTGATGATTATGATGTCATGCAATAAGGAATGACCTGTTCTGGTTCTAC	Induced in Individual 11, but not in Individual 13	AF224669
212	G + AP54	putative DNA-directed RNA polymerase III C11 subunit	142bp	AAGCTTTGAGGTAAAGGCCAGGCGGTAGGAAATATGGCCTATCTGCCAGGCAGGGTGGATGAAGTCATGAATGCTGGAGTTTCTGTGTTGGAGGAGACAGAACCCATAACTAAATATGCTCTGTGTAAGTCC	Induced in Individual 11, but not in Individual 13	AF126531
213	G + AP54	testis-specific kinase 2 (TESK2)	89bp	AAGCTTTGAGGTACAAGTAAGAA GGCTGACCAGCACCTGTAACACTGACTTATTTTAAGTCTGAAAATGTC TTGGAAAAGTTAC	Induced in Individual 11 and Individual 5, but not in Individual 13	NM_007170

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
213	G + AP49	integrin, beta 2 (antigen CD18 (p95)	87bp	GTAATAAAATGGCACACCTTAA TCAGACTGATGTCCCTGACTTGAC AGGAAACACGCACTAACCTCACC ACCTCAAAGCTT	Induced in Individual 11 and Individual 5, but not in Individual 13	NM_000211
214	A + AP49	No significant match to anything	111bp	AAGCTTTAGTCCACCTTACAACAAA GAGCAGCTTGTCTTGAGCTTTG TAGCTCTTAACCTCCAGATTAACT GTGTAGCCATTCTAGTAGCACTAA AGATTAACCT	Induced in Individual 11 and Individual 5, but not in Individual 13	
215	G + AP49	PAC clone RP4-726N20 from 7q32-q34	139bp	AAGCTTTAGTCCAAATTAGGGAGTAA AAGGGGGAAAGGGGCCTATCCATT CCATTGTGGAAAGCTGGGCCAGGTG CCAGGGGACACTCTCCTTCAGGGAA AATGTTATGTGGAGGGAGCAAT AAATTATTTTGTTTTC GGGGAGAAAATGTATCAAAAGGAGT	Induced in Individual 11, but not in Individual 13	AC006344
216	G + AP49	BAC R-487K10 of library RPCI-11 from chromosome 14	133bp	TTATTTAAAGCAATGGTAGTATCAG TCCTAAAGCAAAACACTGGAAACAAA AAAAACACAAAAACCTTTCTCG ATATGAAATCATCGATTATTTGGA CTAAAGCTT	Induced in Individual 11, but not in Individual 13	AL352976
217	G + AP49	F-box protein FBL4 mRNA	100bp	AAGCTTTAGTCCATAATTGATTGA TAAAAGAATAACATGGAAATCATGCT AACTTATTTCAAAGGAACACTGAG CAATAAAAGTATGTGGCATTATGCT	Repressed in Individual 11, not in Individual 13	AF176699

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
218	G + AP11	cDNA DKFZp762H1311	215bp	AAGCTTCGGTAAGGAATGAGAAC TCTGAAATCAGATGGAAAAAGCG GTGTTAATTCTATGGCTGTGATC GTAGCTGTGATAAGGGACTGAGGA ATAAATTGTCGCTTGTCAATGGCA ACCAGCTCTGAAAAGCCCACTGA AAATTGCCGTCCGTGGTAAC GCTACGGGTAAGATTGCCTAA CAGTACTATTCTCGGCCACC	Repressed in Individual 5, not in Individual 13	AL359817
219	G + AP4	cDNA DKFZp434F2021	63bp	GGCTTCAACTACATGTAGGTGTTA ATATGAAAATCTGCCACAGCCTAC CGTTGAGAAGCTT	Repressed in Individual 5, not in Individual 13	AL117573
220				GGTATGTTTAGCAGCACTCTTT TCATCAAATCGGATTATTTAATT TTAGATTTAAATTGTGTTAATAAAAA AGCCCTCATTCATGAGGGCTTTATT TTATGGATGATAAAATTGCTTAACCG TGACGTTTGCAAACCTGTCCATGA AATTAACCAATGCTTGACCCCTTC TAAGGGCACAGCATTGTAATACCT GCACGCATACACCCACAGAGCGA TAAGCTT	Repressed in Individual 5, not in Individual 13	
221	G + AP19	No significant match to anything	233bp	AAGCTTATGCTCATATAATGAGGGCAT CATATCCCTCACTCTCTGGGAC ACATAGCCACTGCCCCCTCCCC GGATGGGAGACTGTGAGGATCCCA GGATTCACTATTCCCTGGCCAGAG GCCCTTGCTGGCTACTGGGTGTT AGTTGGCAGCTGTGCTTCCC TCTCTTATGACTGTGTCCTGGTTG TCAATAAAATATTCCGGC	Repressed in Individual 5, not in Individual 13	NM_006156
221	G + AP19	neural precursor cell expressed, developmentally down-regulated 8 (NEDD8)	239bp			

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
222				AAGCTTCACTAGCTAGACTAATAA GAAGAAAAGAAAAGATCCAATA ACACAATTAGGAATGACAAANGG GATATTACCGNTGACGCCACAAA ATACAAATAACCATCACAGACTATG AACACCTCTATGCACAGAAACTAGA ATTCTAGAAGAAATGGATAAATTG CTGTACAAATNCATCCTCCCATACT GAACCCAGGAGGAATGGATNCNT GAACAGACCAATAATGAGCTCTNA AATGGAAATCAGTNATNAATAGCCTA CTACC	Induced in Individual 5, but not in Individual 13	AL132827
223	BAC C-2149C7		276bp	AGGATCCTCATCAATAGATGAAAC GTATAGGAATAGTCAACTACATCT ACGAAGTGTCAGTATCATGCTGCG GCTTCAAATCCGAAATGATGTTTG ATGTGAAGTGGAAATTTAGTTGTCG TAGTAGACAGACAAATTAGGAAAGTT GAGCCAATAATTACGTGGAAGCTT	Slightly repressed in Individual 11, but not present in anyone else	M27315
224		Rattus norvegicus mitochondrial cytochrome c oxidase subunits I, II and III, and ATPase subunit 6 genes	173bp	AGGGGGGGCTTCGAAGGCCAAAGT GATGTTGGATGTAAGTGAAATAT TAGTTGGGGATGAAGCAGATAGT	Induced in Individual 11 and Individual 5, but not in Individual 13	AF004341
225	A + AP10	cytochrome c oxidase subunit III gene	116bp	GAGGAAGTTGAGCCAAATAATGAC NTGAAGITACGTGGAAAGCTT		
226		No insert - just vector				

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
227		No significant match to anything	322bp	GAGGTTCAACTAACATTATTGC ACAAACTCACTTCAGGCCACTGCTG ACATCCAAAACACAGCCTAGTAA CACACAACCTCACCTCAAGGACT CGAGAGATAAGCCAACCTATATAA ATAATCTCGTGAAACGTAAATTGG GTGAGAAAATATGACCGCTAGAGA CTTTGGCGATGAATAATTGGCTTAG TTCAGAAGGTTGAAAATAACAGTGG CCTACAACTCAAAATTCAACCAAAT AACCGTGGCCCTTAGTCACCCAC CTTCCATCATCTTTACCTCTGCC TGTTCTTGGCCCTTACAGTCGAAGC TT	Induced in Individual 10, but not in Individual 9	
228		No significant match to anything	136bp	AAGCTTCGACTGTACATCATGAA ATCCCTAGGGATCTACTGTATACTA TAGTGACTATAGTTAGTGATACTGT ATAGCATACTGGAAATTCTGAG AGGGTAAATTACATTAAAGTGT TTATCTGGCCC	Repressed in Individual 10, but not in Individual 9	
229	cDNA Y127F12		127bp	AAGCTTCGACTGTAGTACCC ATGGCATTACTTACCATAGCCTAT TGTATTGGCCCTCAAGGCTCCATT GGGCAAATTGTTTTCTATTGTTT AAAGTCAGCACCTAAATCTCCCTG GCC	Repressed in Individual 10, but not in Individual 9	AF075018
230	G + AP2	ribosomal protein L8 (RPL8)	66bp	GGCATAAACACAAACTTATTGAGG CCCTCAGCACTAGTTCTTTCTCC TGGCACAGTGGAAAGCT	Induced in Individual 10, but not in Individual 9	NM_000973

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
231	G + AP4	CGI-51 protein mRNA	371bp	GTTGCTTTAACATTATTGACGGGG TTTCCCCACAGGGGTCCGCAGTCAAA GAATCGCTNGAACCGGGTCTCCTC GAGAGACGGTGTGGCATGGGC GCCCTTGCTGCTGCCCAAGTCCAG AGCTTCTCCGTAGGGGTGCCGC TACAGGAACCTTATCCCAAGCTCCA AACTGGACGCCATCACATATCCTG TCACACTGTCTGTACTCCCATGGGG ACCGAGTAATTAAAGTTCAACCGA GCGATGTTGCCAAGCCTGAGGACCA ATCCCCGGCCCGTACGACCAAGCG GATGCCACTAGCCAGCTTACGAAT ATGAGCTTTGGGGCCCTCCCATATA GTTGAGGTTGCAGGGTTCTGC GTTGAGGAAGCTT	Induced in Individual 10, but not in Individual 9	AF151809
232		BAC clone RP11-357D2 from 7q21.1-q21.2 or cosmid U107D4	228bp	GCATAGGATTGACTTGGCAATGG GGCTCTTTTGGTCCATATGAA TTAAAGTAGTTTCAATTCTG GGAAGAAAGTCATTGGTAGCTTGA TAGGGATGGCATTGAATCTATAAAT TACCTTGGCAGATGCCATTTC ATGATATTGATTCTCCATATCCATG AGCATGGAATGTTTCCATTGTT TGTTATCCCTTTTATTTCGTTGAGA AGCTT	Repressed in Individual 10, but not in Individual 9	AC006374

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
233	G + AP4	ALL 1-fused gene from chromosome 1q (AF1Q)	212bp	GGGATTGAATGTCTTTATAAATAACCGAGTAAATGGTAGCACAAATCACATCAATATTTGGAGGATGGGGACAAGATGTCGAGTCAGATCAGATTATTGTTCAATTCTAGCTGAAGAACGTGCCCCACTGATCAGTATTACGTATTGCAAATGCAGGAGTAAGGGCTAAAATAGGACTTTGCCGTTGAGAAGCTT	Induced in Individual 10, but not in Individual 9	NM_006818
234	G + AP9	BAC R-11K13 of library RPCI-11 from chromosome 14	365bp	AAGCTTCATTCGGTACTCAATTGCTCCCTAAGAGTCAATATTCTGGCATCACACAGATACTAGTATTCTATGTTTTTTCAACTCTAACATTGTAACCTGGAGAGAAACCATCAAATTTTGAGATAACAAAGACTATAGAAAGCATTCACACCTACATAATTAGAAGACTCACATGCACATACCTATGTAATAAGGAAGGAGGGCCGGCGTGGTGGCTCACACCTGTAAATCCCAAACATTGGAGTCCGAGGAAGGTGATCACCCTGAAGTCAGGGAGATGAGACCATCCGGCCAACGTGGTGAACCCCTGTCTTCACTAAATAAC	Repressed in Individual 10, but not in Individual 9	AL355095
235		Insert is too small				
236	G + AP12	BAC R-307P22 of library RPCI-11 from chromosome 14	76bp	AAGCTTGAGTGCTGGCTAGGCCAGAAATTACATTAGCATCCTCTGGTAATTACATTAGTTAGTCCTC	Repressed in Individual 10, but not in Individual 9	AL132777

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
237		clone RP3-505P2 on chromosome 6	281bp	AAGCTTCACTAGTAGAGTAACAA AAAAACGACAATGAGAATGACAA AGGCAATATTGCAACCAAATACCA GAAATACAAAAGTCCCTCAGAGAC TATTATCAACACCTCTATGTGCACA ACTAGAAAATCTAGGGAAATGGA TACATTCTGGAAAGCACACAACTC CCAAGATTGAAATCGGAAGAAATT GAAACCTGAAACAGAACAAATATCAA GTTCCCAAACCTGAATCAGTAATAAA AACCTTAC	Repressed in Individual 10, but not in Individual 9	AL133458
238		No insert - just vector		AACAAGGGAGATCATTTTACCAATTG CATTGGTGTCAGAATAATAGACCCAGA CTTCCCATTCTTACAAGACACTTGTAT TGAGTGCCTACTAAGCTT ATAAAGGGCCAGATAGTAGCTGTGTTG CCACTACTCAACTCTGCCATTGTA TGTAAGTAGTGTCAAGACAAATA TAAGAAAATGAGTGTGACTGTGTT CAATAAAACTTTATTACAAAGCA TCAGTGGGCTGGATTGGCTTT GGCCATAATTAAATCCCTCTGG NAAAATAATCACTATTAGCTGG TCATGAGTACGTGGAAAGCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	
239	A + AP5	No significant match to anything	93bp			
240	A + AP10	No significant match to anything	241bp		Gene is repressed in Individual 10, and not expressed in Individual 9	

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
241	A + AP10	cytochrome c oxidase subunit III gene	183bp	AAGACCCCTCATCAATTGATGGAGA CATACAGAAATAGTCAAACCACATC TACAAAATGCCAGTATCGGGGGC GCCTTCGAAGCCAAAGTGATGTTT GGATGTAAAGTGAATAATTAGTGG CGGATGAAGCAGATAGTGAGAAA GTTGAGGCCAATAATGACCGTGAAG TACGTGGAAAGCTT	Induced in Individual 10, but not in Individual 9	AF004341
242	A + AP19	The size of this gene does not match the autorad	91bp	AGTAAAGGGAGAGAAGGACCTCT GAGGGGGAGAGATAGGGAGTTGA AGCCTGAGCATTAAAGTTCTCTGG AGTGGGGAGCGATAAGCTT	Repressed in Individual 10, but not in Individual 9	
243	A + AP19	ribosomal protein S7 (RPS7)	346bp	ACTGTGAATATACTTTTATTTAG TCATTTTTGTTACAATTGAAACTCT GGAAATTCAAATAAACATCCTTGC CGGTGAGCTCTTATAGACACAG AAAAAGTTCAACCTTGCTTGTCCAAA ATTGTTCTGCTGTGCTTGTCC TGAAACCTTATGAGCCGGATTCTCTTG TCTAGTTGACGGGATTCTCTTG CCACAATTGCTGGAAAGACCA AGTCCTCAAGGATGGCATCGTGCA CAGCTGTCAGAGTACGGCTCCTGG GACGCTTTGGCTTATTTTTGACG GCTTTTCGAGTTGGCTTAAGCAGA ATTCTCCTGAGCGATAAGCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	NM_001011

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
243	A + AP19	No significant match to anything	392bp	GCCTTATCGCTCCTAGGCCTACAAAC CTGGCACAGCATGTTACCGTACTGA AGACTGTAGGCCAGTTGTAACACAA TGTTAAGTATATGTGTATCTAAATA TATCTAAACATAGAACAGGTAAATGC ATTGCACTTAACATTACCTTATGA CAGCCACGACATCTCTAGGTGACA GGAAATTTTTAGCTCTATTAAAGTT TCCTGGGATCACCATTCTATATGTGA TCATCATTTGACTGAAATGTCAATT TGCAAGCAAATTGTATATAACTATT TCATTTGGCCTGCCTAAAAATCTT AGTAGTGTGGGGAGAACCTGATTA GGGATTGTTTAAGGCATATATGGTC AAGCATATGAATTTCAGATATTAT GTTTATGGAAAGACTCCCTTGT	Gene is repressed in Individual 10, and not expressed in Individual 9	
244	C + AP17	No significant match to anything	125bp	AAGCTTACCAAGGTAGGAGAAAATA CTAGAAAAGCACAGCTCCCTGGAG TAGTGGAAATGAATCTATCATCAATA CCATTCCCTACAGTTATTCTGCATTAA AACATGGTACAGTAGGCCAACATA GG	Gene is repressed in Individual 10, and not expressed in Individual 9	AL008722
245	C + AP17	clone CTA-732E4 on chromosome 22q12.1	86bp	CAACATTGTAAAACAGGAATAAAA CCTTCCTTATTTTATCTCCTCT TATCTTGAAACATCTGGCATAGTAC TGTTAAGCTT	Repressed in Individual 10, but not in Individual 9	
246		Insert is too small				
247	C + AP20	UBA3 (UBA3) mRNA	133bp	CAAAATATGATTTTATAATAAT AGTGCAAAAGCATCAGTGATAACT GTTTGAACATTAATTTTTAAACAG CCATGTCTGGCATAGTTAATATT GTGCATATTGGCCTCTATGGCACA ACAAGCTT	Induced in Individual 10, but not in Individual 9	AF046024

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
248	C + AP21	No significant match to anything	92bp	CCAAAAAGAGGCCATGCCCATGCCAGAGGG AAAGTTGGAAAACGAAAGCCAAGTT TTCATTAAAGGAACATTAAGA GGTTAGGCCAGAGAAAGCCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	
248	C + AP21	hypothetical protein (HSPC004)	96bp	CACGGAAACCAAGATAACATTATTAA ATCTACTCTAGGCCGAGCAATAAAG ATGTCTACAGAGTTCACAAACCTGCA ACACTTCACCAAGAGAAAGCTT	Gene is repressed in Individual 10, and not expressed in Individual 9	NM_015918
249	C + AP23	Homo sapiens 12 BAC RP11-575G13	207bp	GCTTGGCTATGAGGACACAAGGC ATAAGAAATGATGCAATGGACATTCA GGACTTGGAGGGATAGAAGAGTGGAG GAGGTGAAGGATAGAAGAGTACAA ATATGGTGCAAGTGTATACTGCTTG GGTGATGGGTGCACCAAATCTCA TAATTCACCACTAAAGAACCTACTT ATGTAACCAAATACCACTGTACCT CAATAACTTATGG	Gene is repressed in Individual 10, and not expressed in Individual 9	AC010200
250	G + AP41	Familial Cylindromatosis cylid gene (hypothetical protein (HSPC057))	241bp	AAGCTTACGGGGTGTACCAAGGG AACAGGCTTTTCAGTGTGTGATGAAGA TTGTGGCGTGTGTTGCATTGGA CAAGCTAGAACTCATAGAAGATGAT GACACTGCATTGGAAAGTGATTAC GCAGGGTCCTGGGGACACAATGCGAG GTGGAACCTCCCTTGGAAATAA ACTCCAGAGTTCTTGAAGGTTGG AGAAACAATAGAATCTGGAACAGTT ATATTCTGTGATGTTTGGC	Induced in Individual 4 and Individual 10, but not in Individual 13	AJ250014

Band	Primer Combination	Identification	Size	Sequence	Expression in Individuals Tested	GenBank Accession number
250	G + AP41	ribosomal protein L8 (RPL8)	218bp	AAGCTTACGGGGTGTGGCCATGAA TCCTGTGGAGCATCCTTTGGAGG TGCAACCACCCAGCACATCGCAA GCCCTCCACCATCCGCAGAGATGC CCCTGCTGGCCGAAAGTGGTCT CATTGCTGCCGGACTGGACG TCTCGGGGAACCAAGACTGTGCA GGAGAAAAGAGAACTAGTGCTGAGG GCCTCAATAANAGTTGTGTTATGC C	Induced in Individual 4 and Individual 10, but not in Individual 13	NM_000973
251	G + AP55	Homo sapiens chromosome 5 clone CTD-2165P17	136bp	AAGCTTACGTTAGGGCGAGAAAAG AGAAGACATTGGTCCCTATTTCACA GTGGATTGACAAAGGTGTTCCGT AGGTAAATAATGTTTGCTGAGAGA TGTCAGTTAGCACAGGAAGCAACA CAGTGGGATTGGCC	Induced in Individual 4, but not in Individual 13	AC010411
252	A + AP47	No significant match to anything	240bp	AGCTAAATAACCATCATTTATGTTAT TAAATAGAAGCCCAATTCTACCTATG TCACTCTAATTCTCTGATCTTGCAA TTTCAACTGTGGTATTACAATATA ATTGTATTATTCATAGACAGCAAGA ATAAAATAAAATAAGTGGGTGAATGA TTACATTTAAAGACATTGTTCTAA GTAGTAATTAGAAAAGGCTATTAA TTAATAATTCTCCAAGTCACCCCC ACGGGCATAAGCTT	Induced in Individual 4, but not in Individual 13	
253	A + AP47	Chromosome 16 BAC clone C17987SK-A-67A1	106bp	AGATATAGAAGTCCCACTAGGGTT CCCTGGCTGGTCTAAACTCTTGG TTTCAAGTGTATCCCTGCCCTGG CCCTCCAAAATGCTGGTATTACGG GCATAAGCTT	Induced in Individual 4, but not in Individual 13	AC004531

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
254	A + AP52	hypothetical protein FLJ20436 (FLJ20436)	204bp	AAGCTTGACCTTGTGGATGATGTT CGTTGCCAATCAGTCTCTCCAA TGACCAAGACACTGCCTTACCCAGA AAGATGCGACTGCCATTGGTGACC TGTTAACCTTAACCTGTGGTCTAAT GGAGACAGACACTCGACTGAAAGTG AAGGACCCAGACTCTAGTTGAACA TAAAAGGATTCCCTCTGTACTAGCAC ACTCCCCCT	Induced in Individual 4 and Individual 10, and only slightly in Individual 13	NM_017822
255	A + AP45	No significant match to anything	187bp	CCACAGAGATAATAAACTCACT AACATTATAAAAATACTTTTCCAAC TACITTTACATGACTTAATGTTTCCA ATTATTTGCGAAACCATGTCGGCG AGGTCTTAGCTGGTCTTGTAAAG ATTCTTAATTTCATTTGGCAATATC TAATTTTATTTACATACATGTGGA CTTAAAGCTT	Induced in Individual 4 and Individual 10, but not in Individual 13	
256	C + AP49	clone TCBA00781	223bp	AGTTAAATGACATTATTCCCTCA GTTGAACAAACCTCTACACAATAAA ATGTTGACTTAAGATCTTTCTTT TTGTGAAGAAATTAGGTCTCAAG AACTTTTATGAACTTGTCTATGAGTA CTTCCTGGAAATCAATTAACTGAGT CTTTGGAAACCCCTAGAGAAGATAG GAGAAAATTGGTTCAGAACGAGCA TTAAATTAAGTCAGCCAAAGCTT	Induced in Individual 4 and Individual 10, but not in Individual 13	AF283772

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
256	C + AP49	No significant match to anything	225bp	AGACAAGAGCATTGCCAGATGTAC TGTTGGATTCCCTCTTACCATGGCA AATTCATAGTGATTTCATTAGA ACGATAAACACAAATTGGTTGTGTT GATGAAAAGGAAAGGGCTTGCTTGA AGTGTGTTGGAGTTTATAGTTT CAAACCTGCAGGAACATGTGGATT GAGACATATAGGAAGTGATTTTT TTCTGTGCTTTAGTCAGCCAAGCTT	Induced in Individual 4 and Individual 10, but not in Individual 13	
256	C + AP49	prothymosin, alpha	224bp	AAGCTGGCTGACAATGAGGTGA CGAAGAAAGGGAAAGAAGGGTGGG AGGAAGAGGGAGGAAGAAAGAA GGTGATGGTGGGAAGAGGGATGGGA GATGAAGATGAGGAAGGCTGACTCA GCTACGGGCCAAGCGGGCAGCTGA AGATGATGAGGGATGACGATGTGCA TACCAAGAAGCAGAACGACCGACGA GGATGACTAGACAGCAAAAGGA AAAGTTAAACT	Induced in Individual 4 and Individual 10, but not in Individual 13	M14483
257	C + AP51	KIAA0874 protein	240bp	AAGCTTCGAAATGCTAGAAAAAT TGGGAATGGAGTATGCTGAAAA GTTTGGATTCAAGAAGAAAAAG GATGGTTAGTTAACATGATGATTCT TTTAAACTCTCAAATATCATGAAAC AAGATACTAAATTGTAACCTAAGGAT TTGTATTCTTACAAATTGTTCTAA ATATCTGTTAACATGACTAGTTGATA TTTGTGCATGTTATTAATAAGAG TTATTTTATAG	Repressed in Individual 4 and Individual 10, but not in Individual 13	AB020681

Band	Primer Combination	Identification	Size	Sequence	Expression In Individuals Tested	GenBank Accession number
258	C + AP49	(a total of 3 matches-equal scores for each) chromosome 5 clone CTD-2284O10, Homo sapiens mRNA; cDNA DKFZp434L1, Homo sapiens cDNA FLJ12597 firs, clone NT2RM4001371	86bp	CAACAGAATAATTATATCCAGG AGATTCTGCCATTTCAGGCCTGG AAAAACAAATGCTCCCTGGAAACTG GACTAAAGCTT	Induced in Individual 10, but not in Individual 13	AC008925
259	C + AP53	No significant match to anything	185bp	AAGCTTCCCTCATGTAAACACAAAC AAATGCAAATGTAGCTCTGCTTCCC TCCCTCCCTATAGTAACACTTAAA ACCATATTTCATAATGATTAAACACTTAAAC GAAAATGAGATTAAACCTGCATTC TTACTTAACAACTATGTATATTGCAGA CATTGGATGCCGTGTACAGAGAT CCTCATATG	Induced in Individual 4, but not in Individual 13	
260	C + AP56	mRNA for KIAA1618 protein, partial cds	192bp	AAGCTTATGAAGGACAGGCACAGC TGTGGACCGATTGCAAGTACAGGG AGAAAGAGGTGAAGAGATAACCTGT GGCAACATCTGAAAAAACACGTGG TACCATTTGGCCTGTGGACTGCC CGGACTTTTGCCCTTGTAGTGG CAGTGAGGAGTAAACTGAAAACAG GCCTGATTGTCCTTTGTAGTGG	Induced in Individual 4 and Individual 10, but not in Individual 13	AB046838

**Table 11**  
**Class Discriminator Genes**

GENE	t-test p-value
5-aminolevulinate synthase 2 [ALAS2]	0.0010
Cide-B [CIDE B]	0.0006
clone RP11-468G5	0.0008
metallothionein-1G [MT1G]	0.0040
NADH oxidoreductase subunit MyoFE	0.0030
Penicillin Band 109-A-2	0.0003
Penicillin Band 117-B-2	0.0050
Penicillin Band 134-A-2	0.0031
Penicillin Band 134-A-4	0.0046
Penicillin Band 149-B-3	0.0037
Penicillin Band 238-A-2	0.0016
Penicillin Band 240-A-4	0.0000
Penicillin Band 244-A-2	0.0001
Penicillin Band 69-B-3	0.0031
Penicillin Band 77-C-2	0.0041
prothymosin, Alpha	0.0019
Rat mitochondrial cyto oxidase I, II, III, and ATPase subunit 6	0.0029
ribosomal protein S2 [RPS21]	0.0014
ribosomal protein S24 [RPS24]	0.0028
ribosomal protein S4, X-linked [RPS4X]	0.0008
ribosomal protein S7 [RPS7]	0.0018

**CLAIMS**

1. A method of identifying hypersensitivity in a subject, the method comprising:
  - 5 obtaining a gene expression profile of genes associated with hypersensitivity of a subject suspected to be hypersensitive; and detecting in the gene expression profile of the subject a predetermined pattern of gene expression of genes associated with hypersensitivity.
- 10 2. The method of claim 1 wherein the pattern of gene expression associated with hypersensitivity is obtained by comparing the gene expression profile of a hypersensitive individual with the gene expression profile of an individual who is not hypersensitive.
- 15 3. The method of claim 1, wherein the genes associated with hypersensitivity comprise at least 2 genes associated with hypersensitivity.
4. The method of claim 1, wherein the genes comprise at least 5 genes associated with hypersensitivity.
- 20 5. The method of claim 1, wherein the genes comprise at least 10 genes associated with hypersensitivity.
6. The method of claim 1, wherein the gene expression profile of the subject 25 that is obtained comprises a profile of levels of mRNA or cDNA.

7. The method of claim 1, wherein the gene expression profile comprises a profile of levels of protein expression.

8. The method of claim 1, wherein expression of the genes predetermined to be associated with hypersensitivity is directly related to prevention or repair of toxic damage at a protein, nucleotide, macromolecule, organelle, tissue, organ or system level.

9. The method of claim 1, wherein the gene expression profile is a profile of nucleic acid expression obtained from a cell or tissue sample, or a protein expression profile derived from cells, tissues, blood, urine or serum.

10. The method of claim 1, wherein the gene expression profile is obtained from a blood, urine or serum sample.

11. The method of claim 1, wherein the method comprises identifying hypersensitivity in the subject to an agent.

12. The method of claim 11, wherein the agent is a pharmaceutical agent.

13. The method of claim 11, wherein the agent is selected from the group consisting of pharmaceutical agents listed in Table 1.

14. The method of claim 1, wherein the genes comprise genes associated with tissues or cells within the digestive system, comprising the liver, pancreas, intestines, colon, rectum, stomach, gallbladder, kidneys or bladder.

15. The method of claim 14, wherein the genes are genes associated with liver toxicity including altered lipid metabolism, fatty liver, cholestasis, jaundice, hepatitis, steatosis, necrosis, hyperplasia, mutagenesis, tumor formation or peroxisome proliferation.

5

16. The method of claim 1, wherein the genes are genes associated with tumor formation, teratogenesis, immunosuppression, pancreatitis, or agranulocytosis.

17. The method of claim 1, wherein the genes are genes associated with cellular manifestations of toxicity.

10

18. The method of claim 17, wherein the plurality of genes comprises genes associated with apoptosis, cell adhesion, autophagocytosis, cell cycle arrest, circadian rhythm, cytokine release, de-differentiation, differentiation, mitochondrial damage, migration, mutation, oncosis, peroxisome proliferation, recombination, senescence, signal refractivity, spreading, or transformation.

15

19. The method of claim 1, wherein the plurality of genes are genes associated with renal toxicity.

20

20. The method of claim 19, wherein the genes comprise genes associated with, necrosis, glomerulitis, nephritis, tumor formation, hyperplasia, proteinuria, renal damage or renal failure.

25

21. The method of claim 1, wherein the genes are genes associated with cardiototoxicity, blood toxicity, skin toxicity, eye toxicity or neurotoxicity.

22. The method of claim 21, wherein the plurality of genes comprises genes associated with tachycardia, arrhythmia, hypotension, hypertension, leukemia, neutropenia, agranulocytosis, peripheral neuropathy, dementia, inflammation, irritation, sensitization, myelosuppression or retinopathy.

5

23. The method of claim 1, wherein the genes associated with hypersensitivity are associated with a specific ethnic group, sex or age group.

24. The method of claim 1, wherein the genes are selected from the group consisting of the genes listed in Tables 3, 4, 5, 6, 8, 10 and 11.

10 25. The method of claim 24, wherein the genes comprises at least 5 genes.

15 26. The method of claim 1, wherein the genes are selected from any one of the group consisting of the genes listed in Table 4.

27. The method of claim 26, wherein the genes comprise at least 5 genes.

20 28. The method of claim 1, wherein the genes are expressed in one or more different cell types within a single tissue or organ.

29. The method of claim 28, wherein the tissue or organ is selected from the group consisting of liver, kidney, lung, heart, pancreas, muscle, brain, testes, ovaries, spleen, stomach, intestines, colon, rectum, eye, and bone.

25

30. The method of claim 29 wherein the cell types are selected from the group of liver cells consisting of Kupfer cells, sinusoidal cells, ito cells, hepatocytes, bile duct epithelial cells, hepatic venule endothelial cells and sinusoidal epithelial cells.

5 31. The method of claim 28 wherein the cell types are selected from the group consisting of the cells listed in Table 9.

32. A method of identifying a number of genes associated with hypersensitivity to an agent, the method comprising:

10 comparing the gene expression profile of cells treated with the agent with the gene expression profile of cells not treated with the agent; and

determining the genes that have altered expression due to exposure to the agent in the treated cells, thereby to identify the genes associated with hypersensitivity to the agent.

15 33. The method of claim 32, wherein the cells comprise cells of one or more different cell types, and wherein each said cell type comprises a gene associated with hypersensitivity to the agent.

20 34. The method of claim 33, wherein said cell types are derived from a single type of tissue or organ.

35. The method of claim 34, wherein said cell types are derived from an organ or a tissue selected from the group consisting of kidney, liver, lung, heart, brain, spleen, thyroid, bone, muscle, intestine, stomach or skin.

25

36. A method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent, the method comprising:

comparing a gene expression profile of one or more cell types of a subject known to be hypersensitive to the agent with the gene expression profile of said cell types in an individual known not to be hypersensitive to the agent; and

5 identifying the genes from said one or more cell types having a pattern of differential gene expression, wherein the pattern of differential gene expression is associated with hypersensitivity to the agent.

37. A method of identifying genes having a pattern of differential gene expression indicative of hypersensitivity to an agent, the method comprising:

10 comparing the gene expression profile of one or more cell types of a subject known to be hypersensitive to the agent before treatment with the agent with the gene expression profile of the one or more cell types of the subject after treatment with the agent; and

identifying genes from said cell types having a pattern of differential gene expression, wherein the pattern of differential gene expression is associated with  
15 hypersensitivity to the agent wherein the samples of multiple individuals are compared in at least six individuals and wherein the results of gene expression profiles are compared statistically using computer software.

38. An array for the identification of a gene expression profile indicative of a hypersensitivity to an agent, the array comprising at least 25 different gene probes, each probe comprising a nucleic acid sequence of a gene associated with the hypersensitivity to the agent, wherein said gene is selected from the group consisting of genes listed in Tables 3, 4, 5 and 6.

25 39. An array of claim 38 wherein the array comprises at least 100 different gene probes.

40. An apparatus for identifying hypersensitivity in a subject comprising:  
a detector for obtaining a gene expression profile of a number of genes associated  
with hypersensitivity of the subject suspected to be hypersensitive; and  
a second detector for identifying in the gene expression profile of the subject a  
5 pattern of gene expression of the genes associated with hypersensitivity, thereby to identify  
hypersensitivity in the subject.

41. The method of claim 11, wherein the method comprises identifying  
hypersensitivity in a subject to multiple agents administered together.

10

42. A method of determining hypersensitivity of a subject to an agent, the method  
comprising:  
obtaining a cell from a subject;  
culturing said cell to obtain a cell culture;  
15 exposing said cell culture to an agent;  
obtaining a gene or protein expression profile of a cell or cells of said exposed  
culture; and  
detecting in said gene or protein expression profile a predetermined pattern of  
expression associated with hypersensitivity to the agent.

20

43. The method of claim 42, wherein the subject is a human being.

44. The method of claim 42, wherein the expression profile of at least 20 genes  
or proteins is obtained.

25

45. The method of claim 44, wherein the expression profile of at least 50 genes  
or proteins is obtained.

46. The method of claim 42, wherein the cell obtained from the subject is a leukocyte.

5

1/14

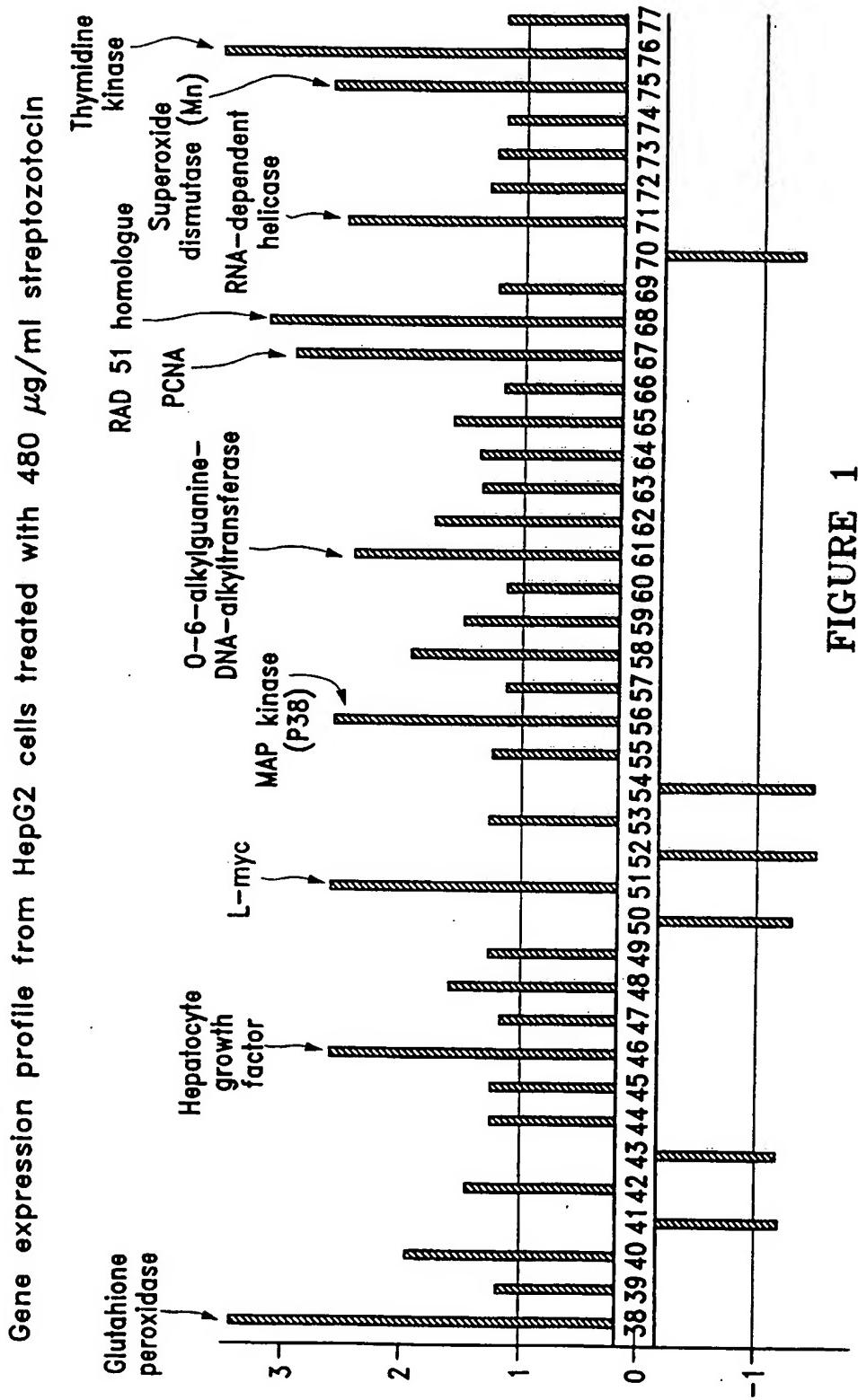
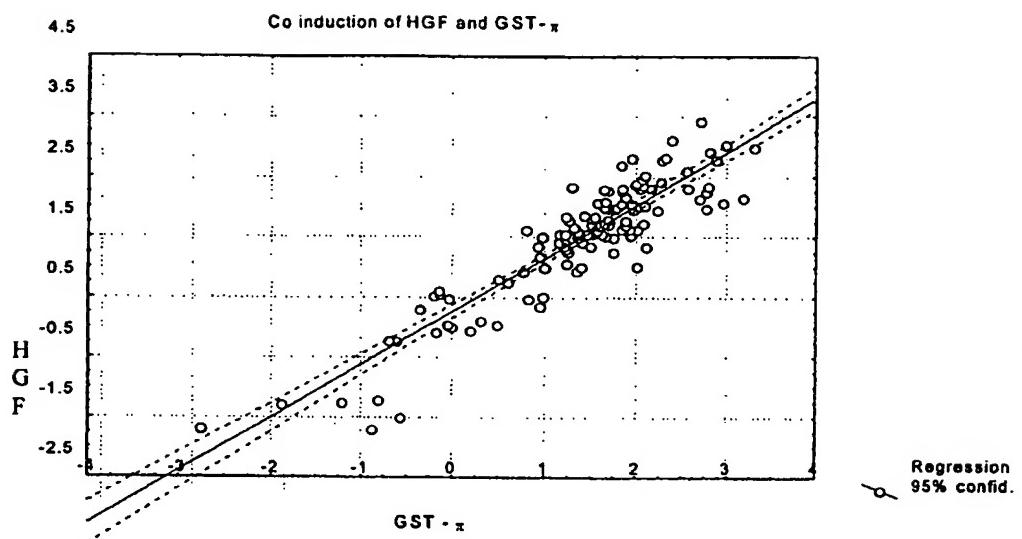


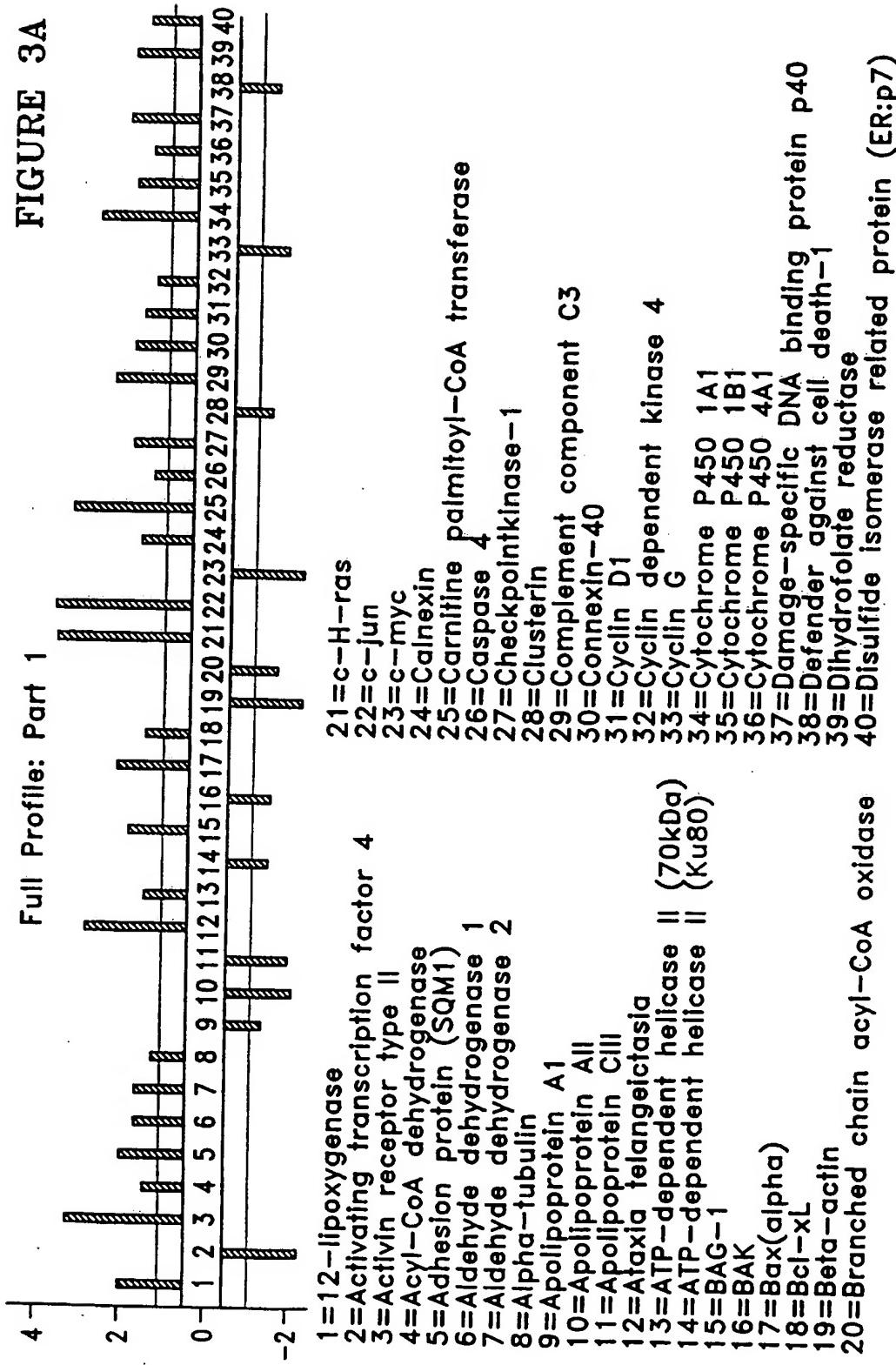
FIGURE 1

2/14

**FIGURE 2**

3/14

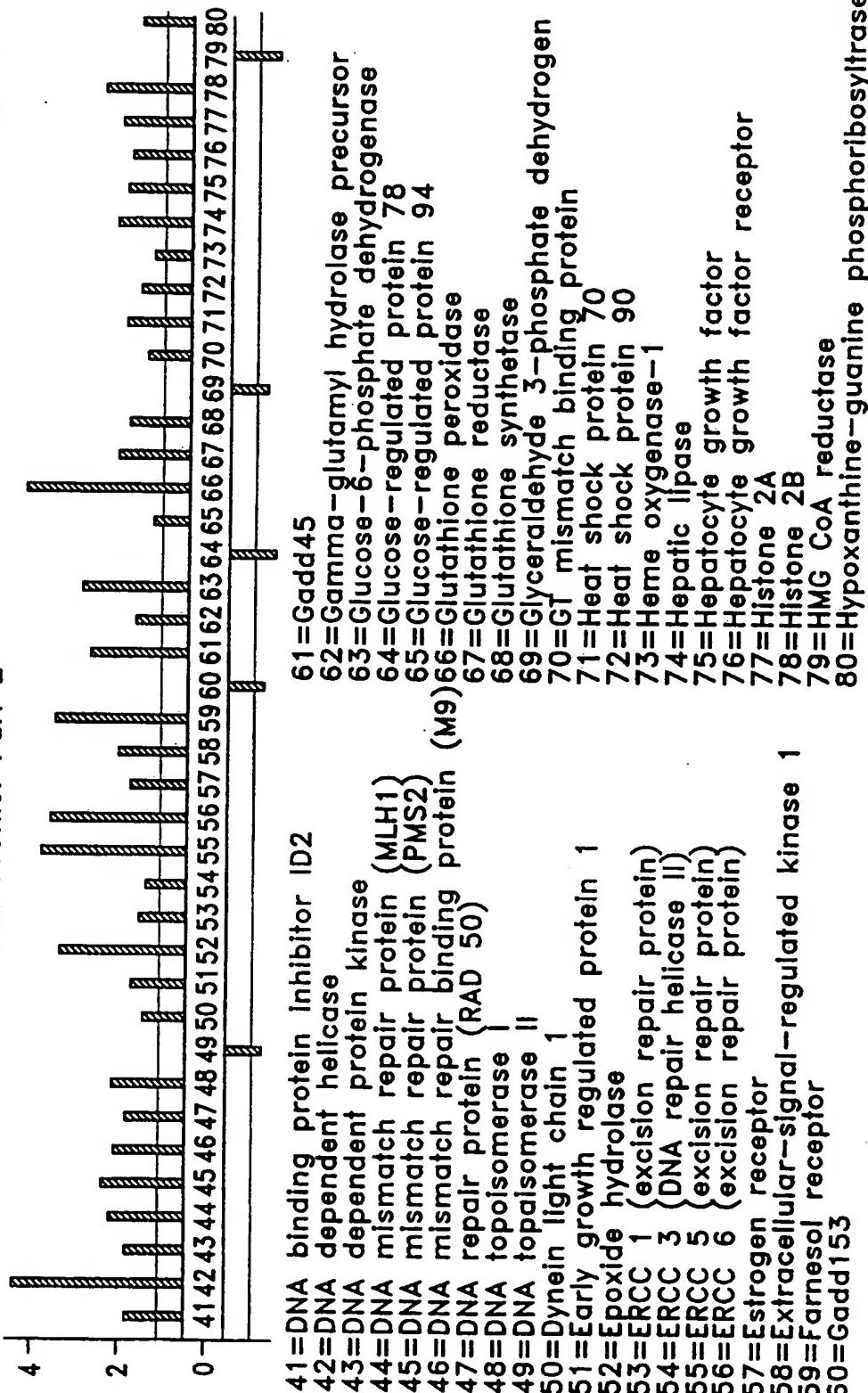
FIGURE 3A



4/14

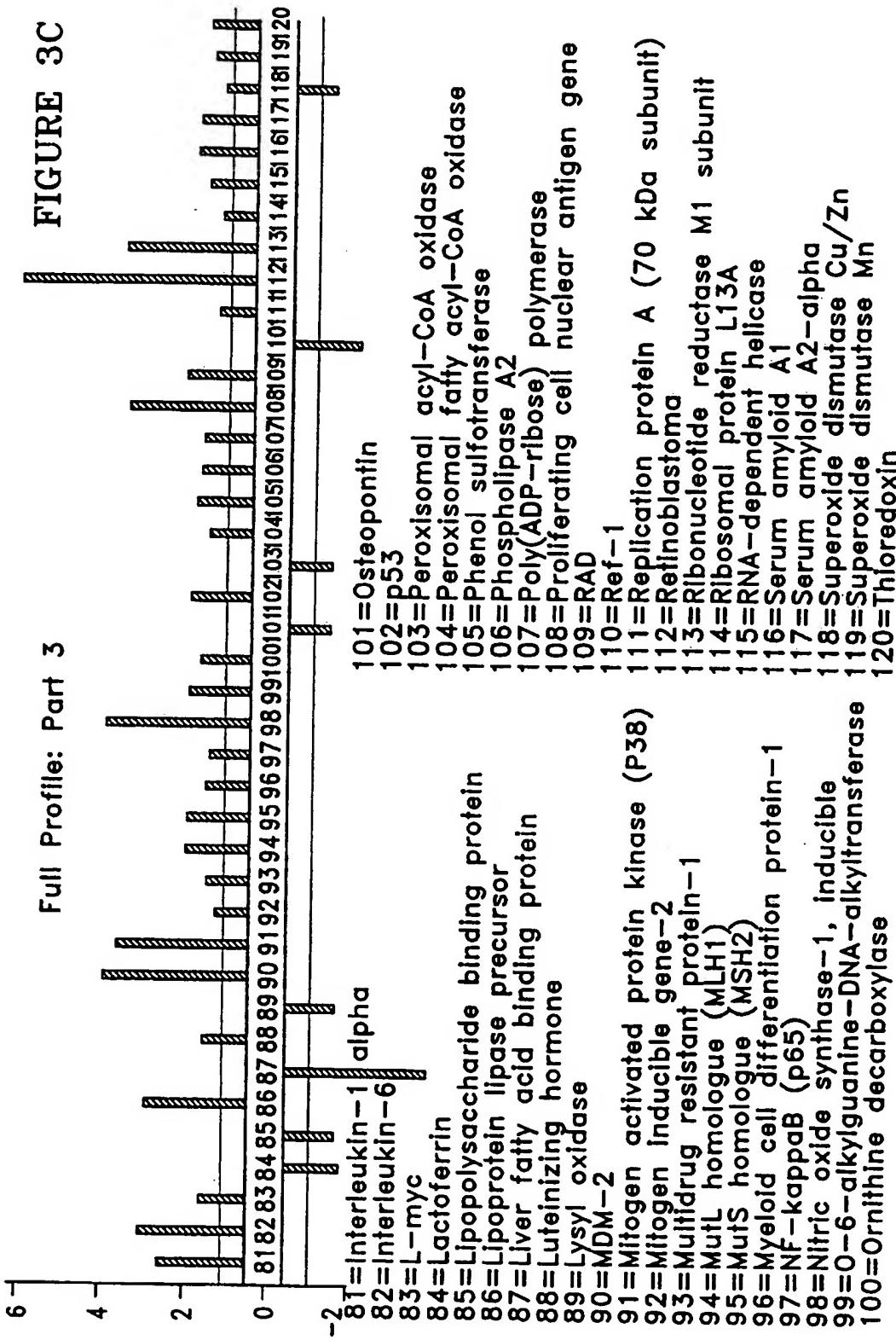
FIGURE 3B

Full Profile: Part 2



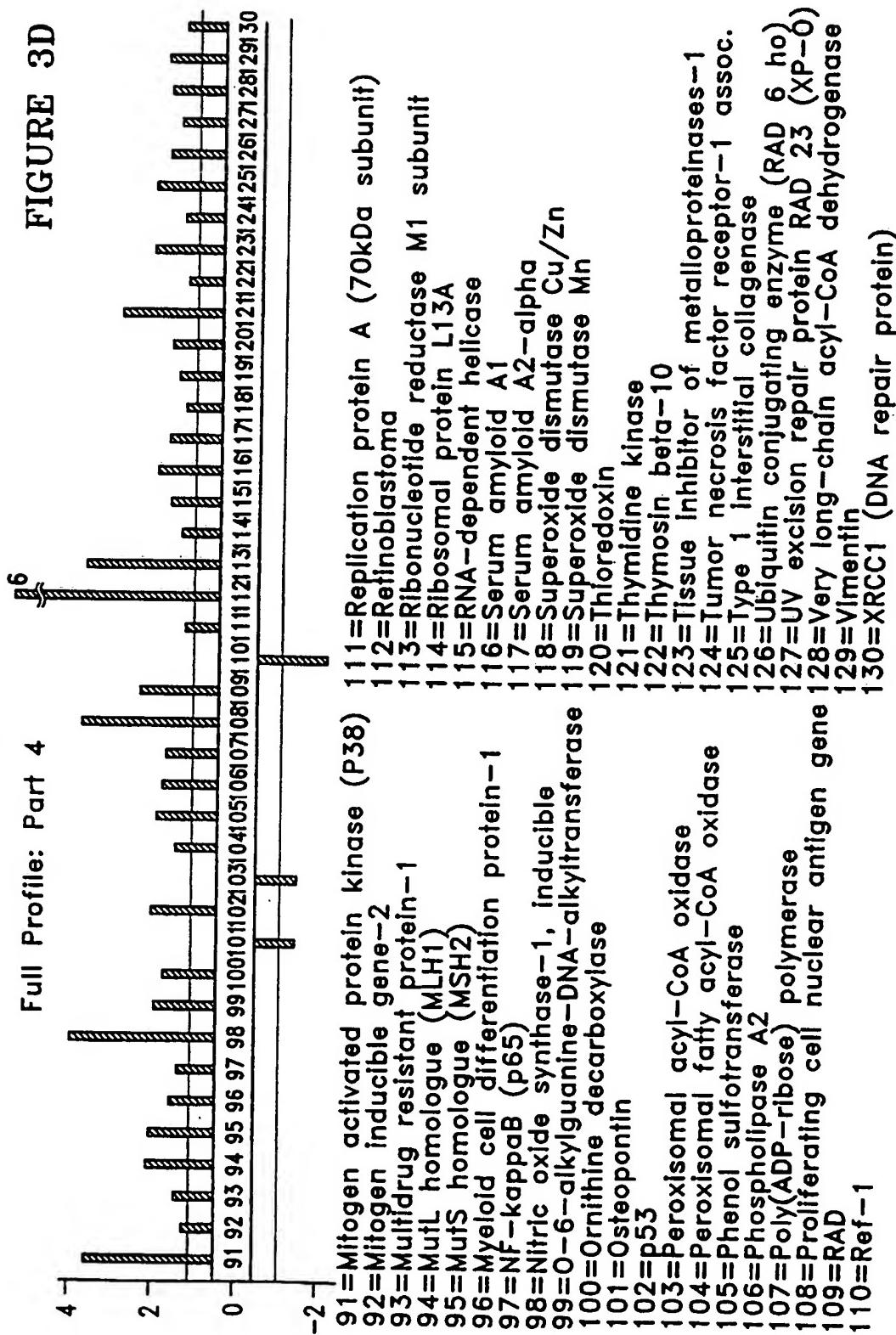
5/14

FIGURE 3C



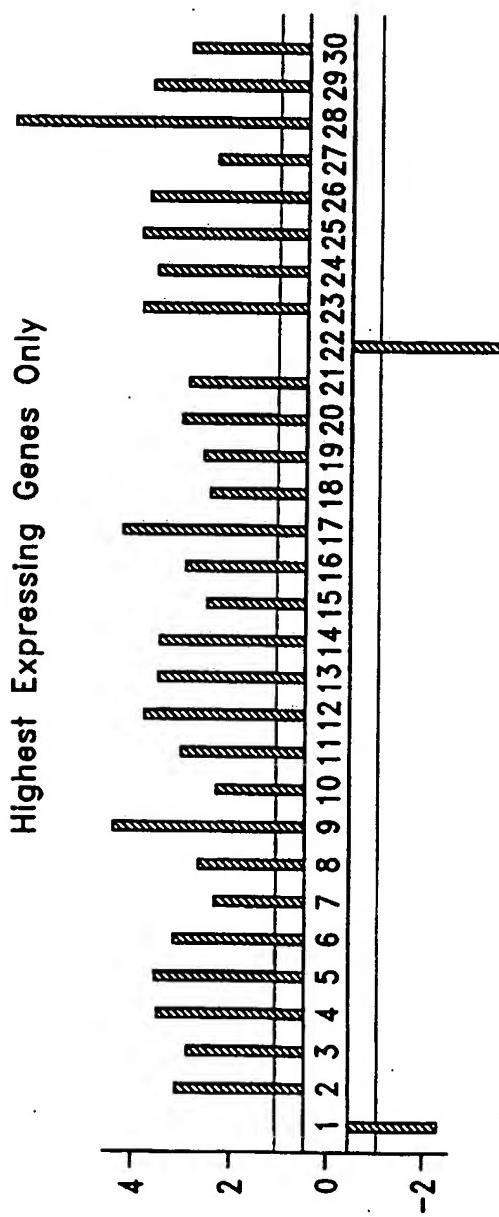
6/14

FIGURE 3D



7/14

FIGURE 3E



- 1=Activating transcription factor 4
- 2=Activin receptor type II
- 3=Ataxia telangiectasia
- 4=c-H-ras
- 5=c-jun
- 6=Carnitine palmitoyl-CoA transferase
- 7=Complement component C3
- 8=Cytochrome P450 1A1
- 9=DNA dependent helicase
- 10=DNA mismatch repair protein (PMS2)
- 11=Epoxide hydrolase
- 12=ERCC 5 (excision repair protein)
- 13=ERCC 6 (excision repair protein)
- 14=Farnesol receptor
- 15=Gadd45
- 16=Glucose-6-phosphate dehydrogenase
- 17=Glutathione peroxidase
- 18=Histone 2B
- 19=Interleukin-1 alpha
- 20=Interleukin-6
- 21=Lipoprotein lipase precursor
- 22=Liver fatty acid binding protein
- 23=MDM-2
- 24=Mitogen activated protein kinase (P38)
- 25=Nitric oxide synthase-1, inducible
- 26=Proliferating cell nuclear antigen gene
- 27=RAD
- 28=Retinoblastoma
- 29=Ribonucleotide reductase M1 subunit
- 30=Thymidine kinase

8/14

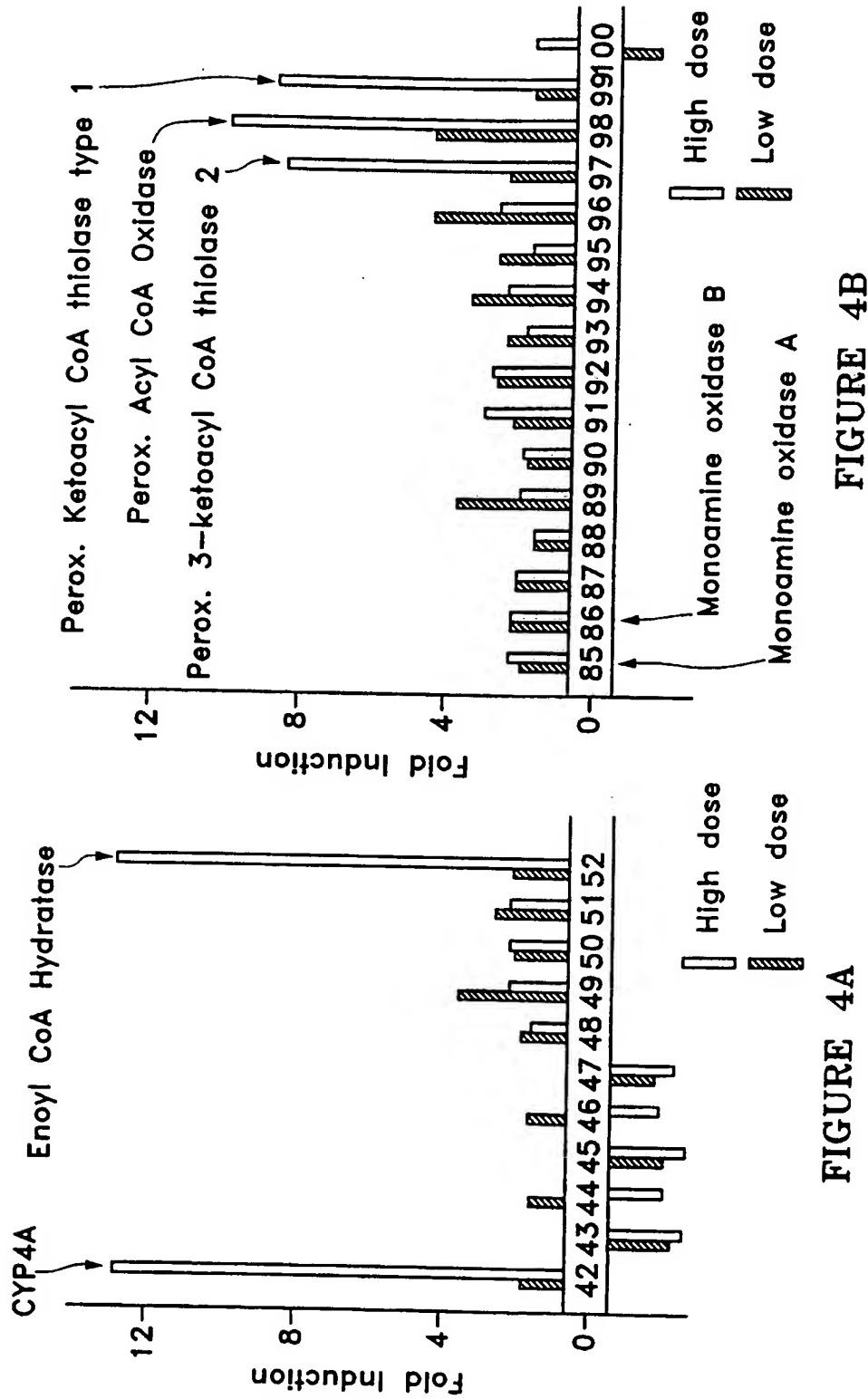
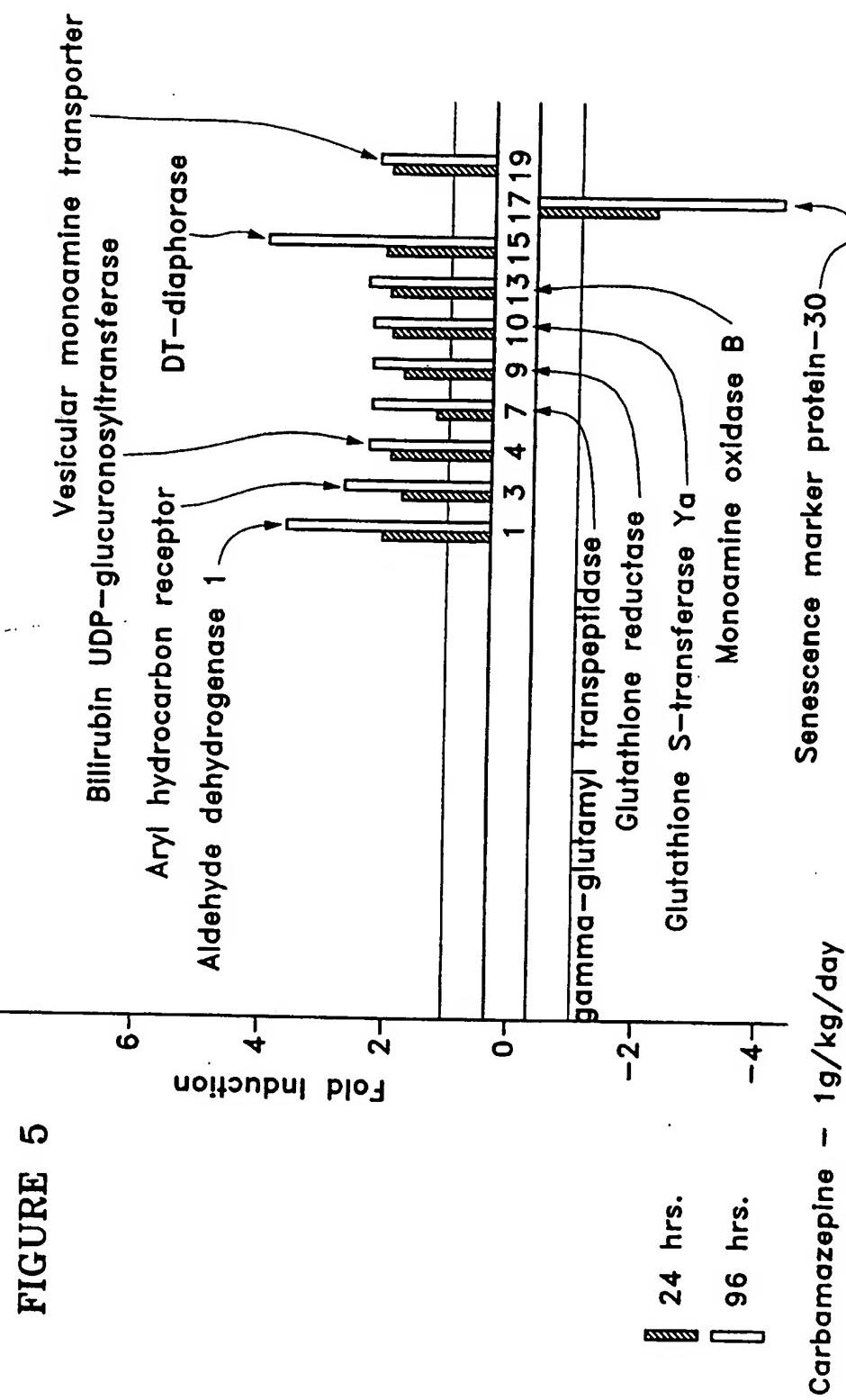


FIGURE 4A

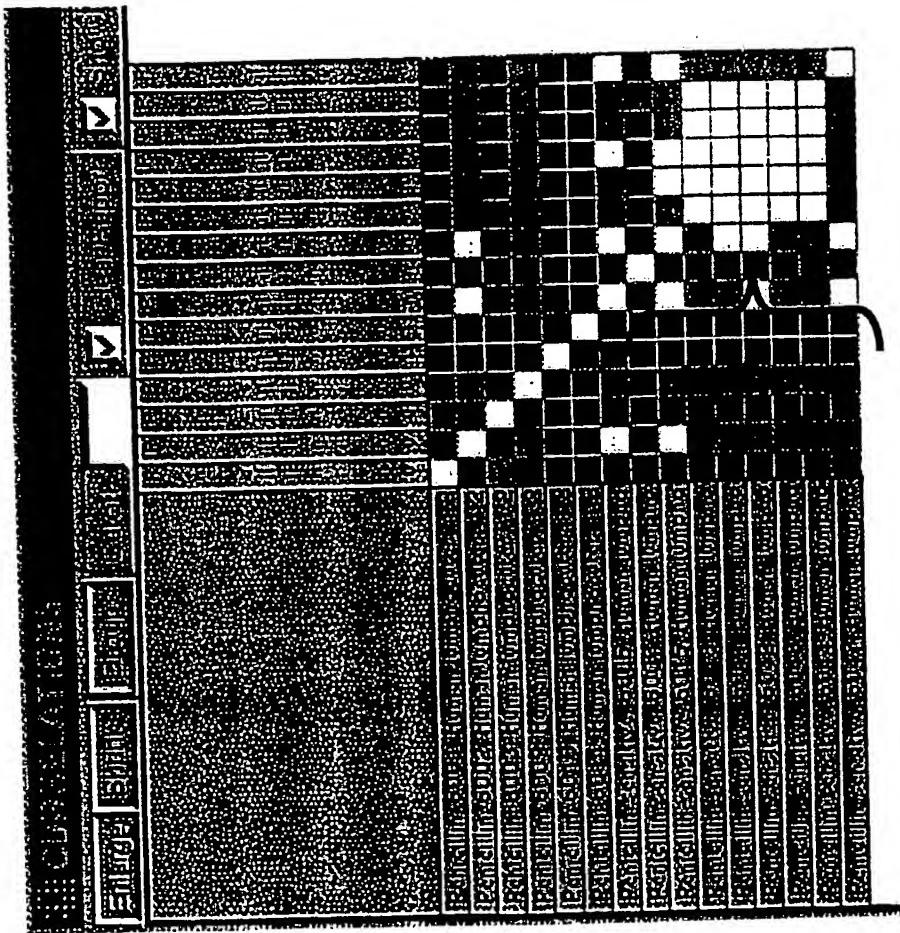
FIGURE 4B

9/14



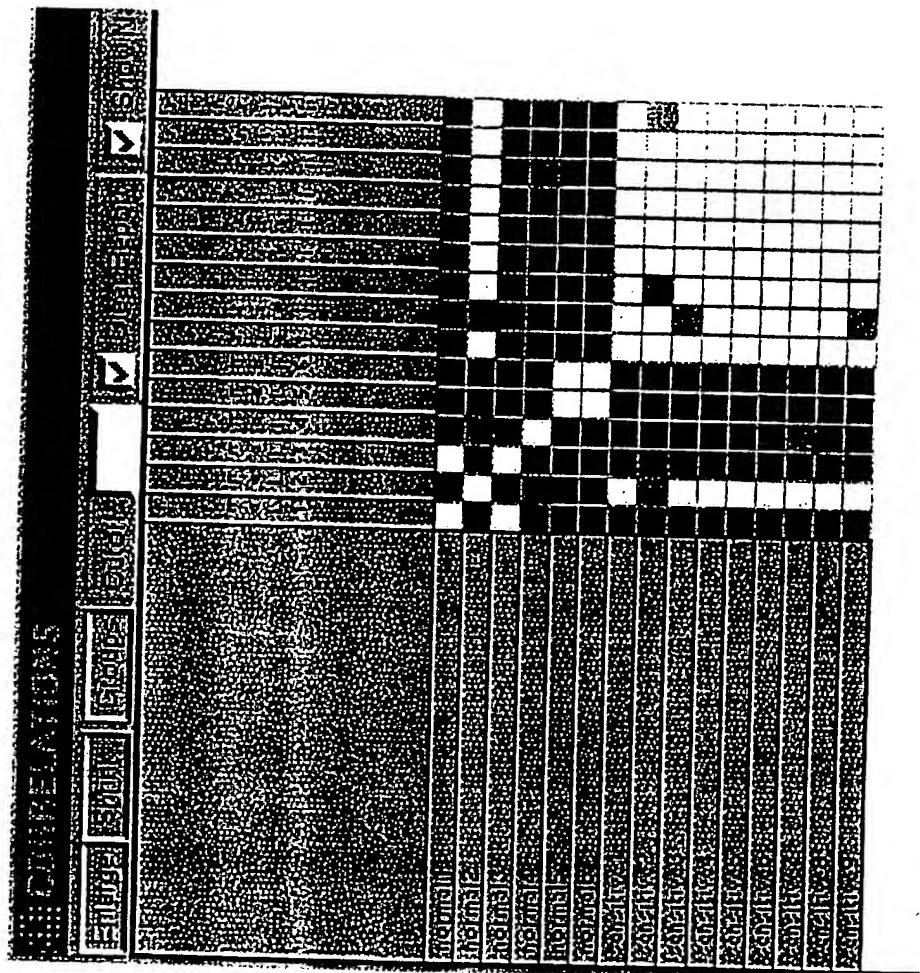
10/14:

*Figure 6*  
*All gene correlation*



11/14

*Figure 7*  
*Discriminator Correlations*



*Figure 8*  
*Inter-Gene Correlations*

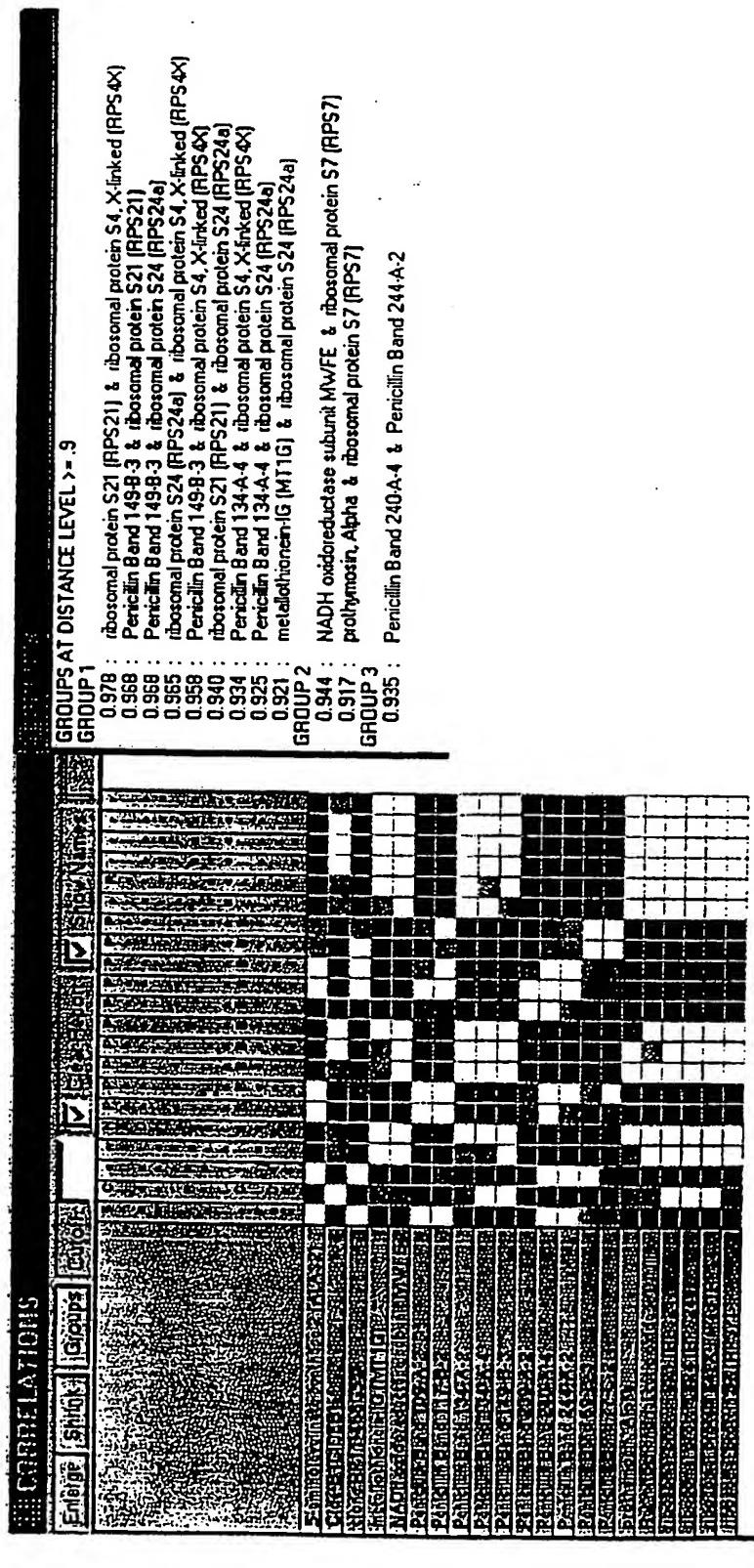
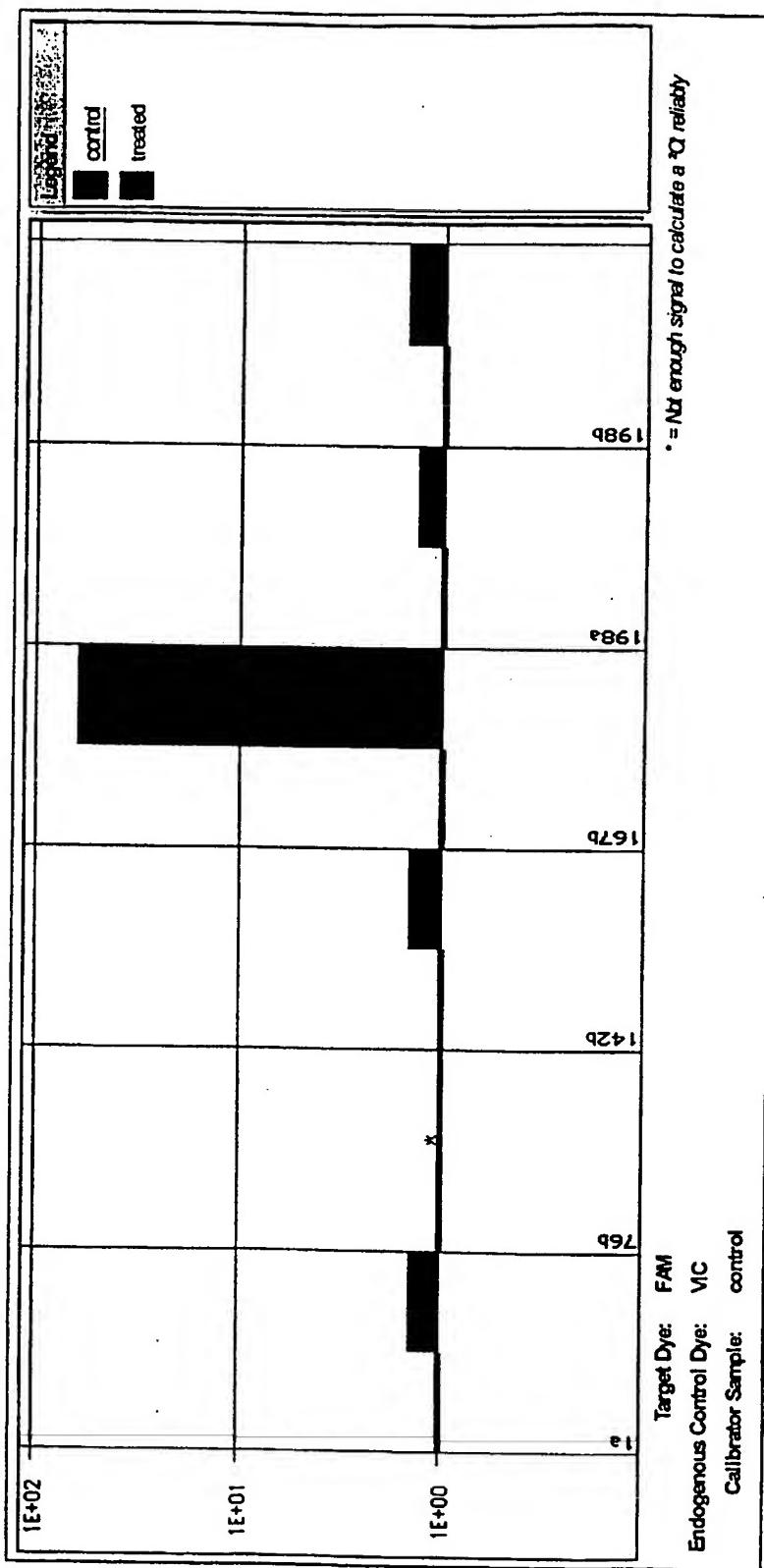


Figure 9 Taqman Results with a Penicillin Sensitive Person



**Figure 10 Taqman Results with a Penicillin Refractive Person**

